ID AAY28444 standard; protein; 1203 AA.
XX
AC AAY28444;
XX
DT 03-DEC-1999 (first entry)
XX
DE Human ptc-2 protein.
XX
KW Patched-2; ptc-2; human; hedgehog receptor; nootropic; neuroprotective;
KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
KW graft; transplant; treatment; nervous system injury; chemical injury;
KW vasal injury; infection; inflammatory; tumor-induced injury; ageing;
KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
KW Parkinson's disease; Huntingdon's chorea; amylotrophic lateral sclerosis;
KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
KW lesion-induced death; neuron regeneration; damage repair; skeletal;
KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
XX
OS Homo sapiens.
XX
PN WO9929854-A1.
XX
PD 17-JUN-1999.
XX
PF 08-DEC-1998; 98WO-US026009.
XX
PR 08-DEC-1997; 97US-0067940P.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Bumcrot DA;
XX
DR WPI; 1999-561298/47.
DR N-PSDB; AAX89478.
XX
PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
PT prevention and/or reduction of the severity of neurological conditions.
XX
PS Claim 3; Page 73-77; 80pp; English.
XX
CC This invention describes a novel recombinantly produced human patched-2
CC (ptc-2) polypeptide which has nootropic, neuroprotective, cardiant,
CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
CC protein is a hedgehog receptor and is therefore capable of modulating
CC hedgehog signalling, and so affect a number of hedgehog-mediated
CC biological activities. The human patched-2 (ptc-2) protein can be used to
CC screen for modulators, antagonists and agonists, which are likely to play
CC an important role in the modulation of cellular proliferation and
CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
CC tissues during disease states. Modulators of ptc-2 protein can be used
CC for in vivo reformation of tissue; to improve grafting and morphology of
CC transplanted tissue; for the treatment, prevention and/or reduction of
CC the severity of neurological conditions deriving from: injury to the
CC nervous system including traumatic injury, chemical injury, vasal injury
CC and deficits (such as ischemia resulting from stroke), together with
CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
CC system including Alzheimer's disease; chronic neurodegenerative diseases
CC of the nervous system including Parkinson's disease, Huntingdon's chorea,
CC amylotrophic lateral sclerosis, as well as spinocerebellar degenerations;
CC and chronic immunological diseases of the nervous system including
CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
CC of autonomic disorders of the peripheral nervous system, including
CC disorders affecting the innervation of smooth muscle and endocrine
CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
CC Antagonists of ptc-2 protein can be used to prevent differentiation of
CC cells in culture, as well as for treatment of chronic pain syndromes.
CC Agonists may be used to rescue neurons from lesion-induced death as well
CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)
CC infection, metabolic disease, nutritional deficiency, toxic agents, and
CC so on. ptc-2 therapeutics may also be used for the repair of central and
CC peripheral nerve damage, for repair and regeneration of non-neuronal
CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
CC for generation of prosthetic cartilage devices, and to induce
CC spermatogenesis and as fertility enhancers. This sequence represents the
CC human ptc-2 protein described in the invention
XX
SQ Sequence 1203 AA;

Pat. 6309379
6605700

Query Match 99.6%; Score 6248; DB 2; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy   61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy  121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy  181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy  241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy  301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy  361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy  421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy  481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy  541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AVMLVFPAIFSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy  601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy  661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy  721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy  781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy  841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWMAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

RESULT 5
AAY92703
ID AAY92703 standard; protein; 1203 AA.
XX
AC AAY92703;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human patched 2 (PTCH2) protein splice variant.
XX
KW Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMM1;
KW familial adenomatous polyposis; hMom1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
XX
OS Homo sapiens.
XX
PN WO200020037-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-SE001784.
XX
PR 06-OCT-1998; 98SE-00003393.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
PI Hollingsworth RE;
XX
DR WPI; 2000-303645/26.
DR N-PSDB; AAA09084.
XX
PT Isolated human protein capable of participating in human patched
PT gene/Sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX
PS Disclosure; Page; 55pp; English.
XX
CC This protein is a splice variant encoded by the novel human patched 2
CC gene (PTCH2), which has been localised by radiation hybrid mapping to
CC chromosome 1p32-35 with D1S211 and WI1404 as closest flanking markers and
CC with an estimated localisation 5.5 cR from D1S443. This region is often
CC lost by LOH in various different tumour types, such as neuroblastoma,
CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour
CC suppressor gene in this region. It is also a candidate gene for
CC involvement in familial melanoma CMM1, modifier locus for familial
CC adenomatous polyposis hMom1 and Michelin Tire Baby Syndrome. PTCH2 is
CC capable of participating in the human patched gene/Sonic hedgehog
CC (PTCH/SHH) pathway during embryonic development and/or carcinogenesis.
CC The isolated human protein is useful as a medicament for the treatment of
CC a condition involving tumours such as BCC (basal cell carcinoma). The
CC nucleic acid is useful in gene therapy, and for use as a probe, primer or
CC a diagnostic agent. Note: This sequence was constructed using information
CC from Figure 2B and the protein sequence given on pages 41-44 of the
CC specification
XX
SQ Sequence 1203 AA;

```
  Query Match             99.5%;  Score 6238;  DB 3;  Length 1203;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1199;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:01 ; Search time 5460 Seconds
(without alignments)
8028.754 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09990046/runat_21112004_130919_18544/app_query.fasta_1.1351
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990046_@CGN_1_1_3361_@runat_21112004_130919_18544 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2724	43.4	3868	9	AY415485	AY415485 Homo sapi
2	2708	43.2	3871	9	AY415487	AY415487 Mus muscu
3	2362	37.7	3950	9	AY415486	AY415486 Pan trogl
4	1097.5	17.5	711	7	CF733501	CF733501 UI-M-HB0-
5	1071	17.1	708	7	CK830937	CK830937 4054508 B
6	1043	16.6	662	7	CF531700	CF531700 UI-M-FY0-
7	1032	16.5	603	7	CN671167	CN671167 A0902E10-
8	1005	16.0	571	4	BM105989	BM105989 509593 MA
9	998	15.9	600	6	CA528868	CA528868 8091-13 M
10	988	15.8	625	7	CN676164	CN676164 A0976A07-
11	970	15.5	911	5	BX844270	BX844270 BX844270
12	959	15.3	974	5	BQ964086	BQ964086 AGENCOURT
13	905	14.4	639	2	BB612664	BB612664 BB612664
14	891	14.2	573	2	BE234509	BE234509 141639 MA
15	884	14.1	778	7	CK639185	CK639185 UI-M-HO0-
16	883	14.1	506	4	BG384338	BG384338 303388 MA
17	881	14.0	796	7	CN537294	CN537294 UI-M-HS0-
18	865	13.8	788	6	CB723145	CB723145 UI-M-GH0-
19	863.5	13.8	832	7	CN536865	CN536865 UI-M-HO0-
20	853.5	13.6	814	7	CN532855	CN532855 UI-M-HO0-
21	844	13.5	633	4	BJ038661	BJ038661 BJ038661
22	839.5	13.4	590	7	CK388757	CK388757 L0933H02-
23	837.5	13.4	746	7	CF741492	CF741492 UI-M-GH0-
24	834.5	13.3	736	1	AU125183	AU125183 AU125183
25	827	13.2	637	4	BJ029994	BJ029994 BJ029994
26	823	13.1	770	7	CK639136	CK639136 UI-M-HO0-
27	818.5	13.1	761	7	CF744664	CF744664 UI-M-GV0-
28	811.5	12.9	711	7	CN535086	CN535086 UI-M-HS0-
29	811.5	12.9	789	6	CB723783	CB723783 UI-M-FY0-
30	810.5	12.9	723	7	CK636036	CK636036 UI-M-HN0-
31	805.5	12.8	812	7	CF745394	CF745394 UI-M-GV0-
32	751.5	12.0	465	5	BQ557141	BQ557141 H4044C10-
33	749	11.9	702	7	CF735093	CF735093 UI-M-HB0-
34	734.5	11.7	637	6	BY727737	BY727737 BY727737
35	732.5	11.7	731	7	CK781271	CK781271 UI-M-GV0-
36	730.5	11.6	659	6	CB722633	CB722633 UI-M-GH0-
37	726.5	11.6	736	7	CN536823	CN536823 UI-M-HS0-
38	712	11.4	589	4	BJ067833	BJ067833 BJ067833
39	711	11.3	477	6	CA530713	CA530713 C0301G07-
40	701.5	11.2	649	7	CN534794	CN534794 UI-M-HS0-
41	701	11.2	751	7	CN535375	CN535375 UI-M-HS0-
42	695	11.1	742	6	CB526181	CB526181 UI-M-FY0-
43	691	11.0	626	7	CO432549	CO432549 UI-M-HX0-
44	679.5	10.8	733	7	CR586364	CR586364 CR586364
45	678	10.8	727	6	CA749673	CA749673 UI-M-FY0-

ALIGNMENTS

RESULT 1
AY415485
LOCUS AY415485 3868 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens PTCH gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY415485
VERSION AY415485.1 GI:39771444
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3868)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3868)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .3868

```
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>3868
                     /gene="PTCH"
                     /locus_tag="HCM5573"
ORIGIN
```

Alignment Scores:

Pred. No.:	1.43e-231	Length:	3868
Score:	2724.00	Matches:	561
Percent Similarity:	59.04%	Conservative:	187
Best Local Similarity:	44.28%	Mismatches:	333
Query Match:	43.43%	Indels:	186
DB:	9	Gaps:	18

US-09-990-046-2 (1-1203) x AY415485 (1-3868)

```
Qy         90 GlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAlaAla 109
Db          3 GGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCTATG 62

Qy        110 TyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrPro 129
Db         63 TTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACCACA 122

Qy        130 GluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeu 149
Db        123 GAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATACATG 182

Qy        150 TyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIleGlu 169
Db        183 TACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACAGAA 242

Qy        170 AsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrProLeu 189
Db        243 ACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCTTTG 302

Qy        190 AspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgPro 209
Db        303 GACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAACCT 362

Qy        210 AspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe--- 228
Db        363 CCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATAAAC 422

Qy        229 AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrVal 248
Db        423 TATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTACATG 482

Qy        249 GlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHisHis 268
Db        483 GACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAAAAT 542

Qy        269 SerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHis 288
Db        543 TCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCCAGA 602

Qy        289 LysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGly 308
Db        603 AAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACTGGA 662

Qy        309 GluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeu 328
Db        663 AAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAAATG 722

Qy        329 TyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGluGln 347
Db        723 TACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGACAAA 779

Qy        348 AlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeu 367
Db        780 GCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGTGTC 839

Qy        368 ProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeu 387
Db        840 GCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATCCTG 899

Qy        388 HisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAla 407
Db        900 AAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGNNNNNN 959

Qy        408 TyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeu 427
Db        960 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1019

Qy        428 AlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeu 447
Db       1020 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1079

Qy        448 GlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGly 467
Db       1080 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTTTGCCATTTCTCGCTCTTGGTGTTGGT 1139

Qy        468 ValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------Thr 485
Db       1140 GTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGAATC 1199

Qy        486 ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeuThr 505
Db       1200 CCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTCACG 1259

Qy        506 SerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArg 525
Db       1260 TCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTGCGG 1319

Qy        526 AlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuVal 545
Db       1320 GCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTCATT 1379

Qy        546 ProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspValLeu 565
Db       1380 TTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATTTTC 1439

Qy        566 CysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGly 585
Db       1440 TGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTACACC 1499

Qy        586 Asp---------------------GlyThrValProValGlyIleAlaHis--------- 595
Db       1500 GACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTTGCC 1559

Qy        596 ------------------LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSer 609
Db       1560 CATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCCCAC 1619

Qy        610 SerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro------ 627
Db       1620 ACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTCACC 1679

Qy        628 ------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAspLeu 645
Db       1680 GTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGACCTG 1739

Qy        646 LeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArg 665
Db       1740 CTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACGAAG 1793

Qy        666 TrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAla 685
Db       1794 TGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAAGCC 1853

Qy        686 LysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThr 705
Db       1854 AAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACCACC 1913
```

```
Qy       706 LeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAla 725
Db      1914 CGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATATGAC 1973

Qy       726 PheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGly 745
Db      1974 TTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAGAAA 2033

Qy       746 GlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSer 765
Db      2034 GCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGTAAC 2090

Qy       766 LeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyr 785
Db      2091 GTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTACTTC 2150

Qy       786 ArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIle 805
Db      2151 AGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAAATC 2210

Qy       806 ThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIle 825
Db      2211 ATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTGGTG 2270

Qy       826 GlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVal 845
Db      2271 CAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTGGTG 2330

Qy       846 AspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSer 865
Db      2331 GATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTCAGC 2390

Qy       866 SerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrp 885
Db      2391 AACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAATGG 2450

Qy       886 LeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPro 904
Db      2451 GTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAGCCC 2510

Qy       905 LeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheVal 924
Db      2511 ATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGCTTGCGGGACACCTCAGACTTTGTG 2570

Qy       925 GluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAla 944
Db      2571 GAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCCAGT 2630

Qy       945 TyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPhe 964
Db      2631 TACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGGCTG 2690

Qy       965 LeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeu 984
Db      2691 CTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTG 2750

Qy       985 AsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPhe 1004
Db      2751 AACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTC 2810

Qy      1005 GlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAla 1024
Db      2811 GGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATCGCT 2870

Qy      1025 SerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGln 1044
Db      2871 TCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCCATC 2930

Qy      1045 GlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAsp 1064
Db      2931 GGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTGGAT 2990

Qy      1065 GlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIle 1084

Db      2991 GGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTCATT 3050

Qy      1085 Val---------------------------------------------------------- 1085
Db      3051 GTCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3110

Qy      1086 ---------ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHis 1102
Db      3111 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGTCTCCAGCCAAC 3170

Qy      1103 GlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluValIleGln 1122
Db      3171 GGCTTGAACCGCCTGCCCACA------CCCTCCCCTGAGCCACCCCCCAGCGTGGTCCGC 3224

Qy      1123 MetTyr------------------------------------------------------ 1124
Db      3225 TTCGCCATGCCGCCCGGCCACACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGT 3284

Qy      1124 ---------------------------------------------------------- 1124
Db      3285 TCCCAGACGACAGTGTCAGGCCTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGC 3344

Qy      1124 ---------------------------------------------------------- 1124
Db      3345 GCGGGAGGCCCTGCCCACCAAGTGATCGTGGAAGCCACAGAAAACCCCGTCTTCGCCCAC 3404

Qy      1125 ----------------------------------------------------LysGluSerPro 1128
Db      3405 TCCACTGTGGTCCATCCCGAATCCAGGCATCACCCACCCTCGAACCCGAGACAGCAGCCC 3464

Qy      1129 GluIleLeuSer---------ProProAlaProGlnGly---------------------- 1138
Db      3465 CACCTGGACTCAGGGTCCCTGCCTCCCGGACGGCAAGGCCAGCAGCCCCGCAGGGACCCC 3524

Qy      1139 ------GlyGlyLeu------------------------------------------- 1141
Db      3525 CCCAGAGAAGGCTTGTGGCCACCCCCCTACAGACCGCGCAGAGACGCTTTTGAAATTTCT 3584

Qy      1142 ---------------------------------ArgTrpGly---------------- 1144
Db      3585 ACTGAAGGGCATTCTGGCCCTAGCAATAGGGCCCGCTGGGGCCCTCGCGGGGCCCGTTCT 3644

Qy      1145 -----------------------------AlaSerSerSerLeuProGlnSerPheAla 1154
Db      3645 CACAACCCTCGGAACCCAGCGTCCACTGCCATGGGCAGCTCCGTGCCCGGCTACTGCCAG 3704

Qy      1155 ArgValThrThr--------------SerMetThrValAlaIleHisProProProLeu 1169
Db      3705 CCCATCACCACTGTGACGGCTTCTGCCTCCGTGACTGTCGCCGTGCACCCGCCGCCTGTC 3764

Qy      1170 ProGlyAlaTyrIleHisPro 1176
Db      3765 CCTGGGCCTGGGCGGAACCCC 3785
```

RESULT 2
AY415487

```
LOCUS       AY415487               3871 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus PTCH gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415487
VERSION     AY415487.1  GI:39771446
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3871)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
```

gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3871)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .3871
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1. .>3871
/gene="PTCH"
/locus_tag="HCM5573"
ORIGIN

Alignment Scores:

Pred. No.:	3.85e-230	Length:	3871
Score:	2708.00	Matches:	569
Percent Similarity:	60.31%	Conservative:	177
Best Local Similarity:	46.00%	Mismatches:	330
Query Match:	43.18%	Indels:	162
DB:	9	Gaps:	17

US-09-990-046-2 (1-1203) x AY415487 (1-3871)

```
Qy        90 GlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAlaAla 109
Db         3 GGTGGACGAGTGAGTCGAGAATTAAATTATACCCGTCAGAAGATAGGAGAAGAGGCTATG 62

Qy       110 TyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrPro 129
Db        63 TTTAATCCTCAACTCATGATACAGACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACA 122

Qy       130 GluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeu 149
Db       123 GAGGCTCTCCTGCAACACCTGGACTCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATG 182

Qy       150 TyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIleGlu 169
Db       183 TATAACAGGCAATGGAAGTTGGAACATTTGTGCTACAAATCAGGGGAACTTATCACGGAG 242

Qy       170 AsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrProLeu 189
Db       243 ACAGGTTACATGGATCAGATAATAGAATACCTTTACCCTTGCTTAATCATTACACCTTTG 302

Qy       190 AspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgPro 209
Db       303 GACTGCTTCTGGGAAGGGGCAAAGCTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCT 362

Qy       210 AspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe--- 228
Db       363 CCTTTACGGTGGACAAACTTTGACCCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAAC 422

Qy       229 AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrVal 248
Db       423 TACCAAGTGGACAGCTGGGAGGAAATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATG 482

Qy       249 GlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHisHis 268
Db       483 GACCGGCCTTGCCTCAACCCAGCCGACCCAGATTGCCCTGCCACAGCCCCTAACAAAAAT 542

Qy       269 SerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHis 288
Db       543 TCAACCAAACCTCTTGATGTGGCCCTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGG 602

Qy       289 LysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGly 308
Db       603 AAGTATATGCATTGGCAGGAGGAGTTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGA 662

Qy       309 GluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeu 328
Db       663 AAACTTGTCAGCGCTCACGCCCTGCAAACCATGTTCCAGTTAATGACTCCCAAGCAAATG 722

Qy       329 TyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGluGln 347
Db       723 TATGAACACTTCAGGGGCTACGACTATGTCTCTCAC---ATCAACTGGAATGAAGACAGG 779

Qy       348 AlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeu 367
Db       780 GCAGCCGCCATCCTGGAGGCCTGGCAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTC 839

Qy       368 ProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeu 387
Db       840 GCCCCAAACTCCACTCAAAAGGTGCTTCCCTTCACAACCACGACCCTGGACGACATCCTA 899

Qy       388 HisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAla 407
Db       900 AAATCCTTCTCTGATGTCAGTGTCATCCGAGTGGCCAGCGGCTACCTACTGATGNNNNNN 959

Qy       408 TyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeu 427
Db       960 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1019

Qy       428 AlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeu 447
Db      1020 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1079

Qy       448 GlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGly 467
Db      1080 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTTTGCCGTTTCTTGCTCTTGGTGTTGGT 1139

Qy       468 ValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------Thr 485
Db      1140 GTGGATGATGTCTTCCTCCTGGCCCATGCATTCAGTGAAACAGGACAGAATAAGAGGATT 1199

Qy       486 ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeuThr 505
Db      1200 CCATTTGAGGACAGGACTGGGGAGTGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACC 1259

Qy       506 SerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArg 525
Db      1260 TCCATCAGCAATGTCACCGCCTTCTTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGA 1319

Qy       526 AlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuVal 545
Db      1320 GCGTTCTCCCTCCAGGCTGCTGTGGTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATT 1379

Qy       546 PheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspValLeu 565
Db      1380 TTTCCTGCAATTCTCAGCATGGATTTATACAGACGTGAGGACAGAAGATTGGATATTTTC 1439

Qy       566 CysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGly 585
Db      1440 TGCTGTTTCACAAGCCCCTGTGTCAGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACA 1499

Qy       586 AspGly-ThrValProValGlyIleAla---------HisLeuThrAlaThrValGln-- 601
Db      1500 GAGCCTCACAGTAACACCCGGTACAGCCCCCCACCCCCATACACCAGCCACAGCTTCGCC 1559

Qy       602 ----------------------------AlaPheThrHisCysGluAlaSerSerGlnHi 612
Db      1560 CACGAAACCCATATCACTATGCAGTCCACCGTTCAGCTCCGCACAGAGTATGACCCTCAC 1619

Qy       612 sValValThrIleLeuProProGlnAlaHis--------------------LeuValPr 625
Db      1620 ACGCACGTGTACTACACCACCGCCGAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACC 1679

Qy       625 oProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAspLe 645
```

```
Db      1680 GTCACCCAG-GACAACCTCAGCTGTCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCT 1738
Qy       645 uLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaAr 665
Db      1739 GCTCTCCCAGTTCTCAGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGCACCAA 1792
Qy       665 gTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAl 685
Db      1793 GTGGACACTCTCTTCGTTTGCAGAGAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGC 1852
Qy       685 aLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaTh 705
Db      1853 CAAGGTTGTGGTAATCCTTCTTTTCCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCAC 1912
Qy       705 rLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAl 725
Db      1913 CCGAGTGAGAGACGGGCTGGACCTCACGGACATTGTTCCCCGGGAAACCAGAGAATATGA 1972
Qy       725 aPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGl 745
Db      1973 CTTCATAGCTGCCCAGTTCAAGTACTTCTCTTTCTACAACATGTATATAGTCACCCAGAA 2032
Qy       745 yGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSe 765
Db      2033 AGCA---GACTACCCGAATATCCAGCACCTACTTTACGACCTTCATAAGAGTTTCAGCAA 2089
Qy       765 rLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTy 785
Db      2090 TGTGAAGTATGTCATGCTGGAGGAGAACAAGCAACTTCCCCAAATGTGGCTGCACTACTT 2149
Qy       785 rArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIl 805
Db      2150 TAGAGACTGGCTTCAAGGACTTCAGGATGCATTTGACAGTGACTGGGAAACTGGGAGGAT 2209
Qy       805 eThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIl 825
Db      2210 CATGCCAAACAATTATAAAAATGGATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGT 2269
Qy       825 eGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVa 845
Db      2270 GCAGACTGGCAGCCGAGACAAGCCCATCGACATTAGTCAGTTGACTAAACAGCGTCTGGT 2329
Qy       845 lAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSe 865
Db      2330 AGACGCAGATGGCATCATTAATCCGAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAG 2389
Qy       865 rSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTr 885
Db      2390 CAACGACCCTGTAGCTTACGCTGCCTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTG 2449
Qy       885 pLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPr 904
Db      2450 GGTCCATGACAAAGCCGACTACATGCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCC 2509
Qy       904 oLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheVa 924
Db      2510 CATCGAGTACGCTCAGTTCCCTTTCTACCTCAACGGCCTACGAGACACCTCAGACTTTGT 2569
Qy       924 lGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAl 944
Db      2570 GGAAGCCATAGAAAAAGTGAGAGTCATCTGTAACAACTATACGAGCCTGGGACTGTCCAG 2629
Qy       944 aTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPh 964
Db      2630 CTACCCCAATGGCTACCCCTTCCTGTTCTGGGAGCAATACATCAGCCTGCGCCACTGGCT 2689
Qy       964 eLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLe 984
Db      2690 GCTGCTATCCATCAGCGTGGTGCTGGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCT 2749
Qy       984 uAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPh 1004
Db      2750 GAACCCCTGGACGGCCGGGATCATTGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTT 2809
Qy      1004 eGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAl 1024
Db      2810 TGGCATGATGGGCCTCATTGGGATCAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGC 2869
Qy      1024 aSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGl 1044
Db      2870 ATCTGTTGGCATCGGAGTGGAGTTCACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCAT 2929
Qy      1044 nGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAs 1064
Db      2930 TGGGGACAAGAACCACAGGGCTATGCTCGCTCTGGAGCACATGTTTGCTCCCGTTCTGGA 2989
Qy      1064 pGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIl 1084
Db      2990 CGGTGCTGTGTCCACTCTGCTGGGTGTACTGATGCTTGCAGGGTCCGAATTTGATTTCAT 3049
Qy      1084 eVal---------------------------------------------------------- 1085
Db      3050 TGTCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3109
Qy      1086 ----------ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHi 1102
Db      3110 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGTCTCCAGCCAA 3169
Qy      1102 sGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluValIle-- 1121
Db      3170 TGGCCTAAACCGACTGCCCACT------CCTTCGCCTGAGCCGCCCCCAAGTGTCGTCCG 3223
Qy      1121 ---------------------------------------------------------- 1121
Db      3224 GTTTGCCGTGCCTCCTGGTCACACGAACAATGGGTCTGATTCCTCCGACTCGGAGTACAG 3283
Qy      1121 ---------------------------------------------------------- 1121
Db      3284 CTCTCAGACCACGGTGTCTGGCATCAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGG 3343
Qy      1122 -------------------GlnMetTyrLysGluSerProGlu-IleLeuSerProProA 1135
Db      3344 TGCCGGAGGCCCTGCCCACCAAGTGATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCG 3403
Qy      1135 laPro---------------------------------------------------------- 1136
Db      3404 GTCCACTGACGGCAAGGCCAGCAGCCTCGAAGGGATCCCCCTAGAGAAGGCTTGCGGCCA 3463
Qy      1136 ---------------------------------------------------------- 1136
Db      3464 CCCCCCTACAGACCGCGCAGAGACGCTTTTGAAATTTCTACTGAAGGGCATTCTGGCCCT 3523
Qy      1137 --GlnGlyGlyGlyLeuArg------TrpGly-AlaSer---------------------- 1146
Db      3524 AGCAATAGGGACCGCTCAGGGCCCCGTGGGGCCCGTTCTCACAACCCTCGGAACCCAACG 3583
Qy      1147 ---------------SerSerLeuProGlnSerPheAlaArgValThrThr--------- 1158
Db      3584 TCCACCGCCATGGGCAGCTCTGTGCCCAGCTACTGCCAGCCCATCACCACTGTGACGGCT 3643
Qy      1159 ------SerMetThrValAlaIleHisProProProLeuProGly 1171
Db      3644 TCTGCTTCGGTGACTGTTGCTGTGCATCCCCCGCCTGGACCTGGG 3688
```

RESULT 3
AY415486
LOCUS AY415486 3950 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes PTCH gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY415486
VERSION AY415486.1 GI:39771445
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

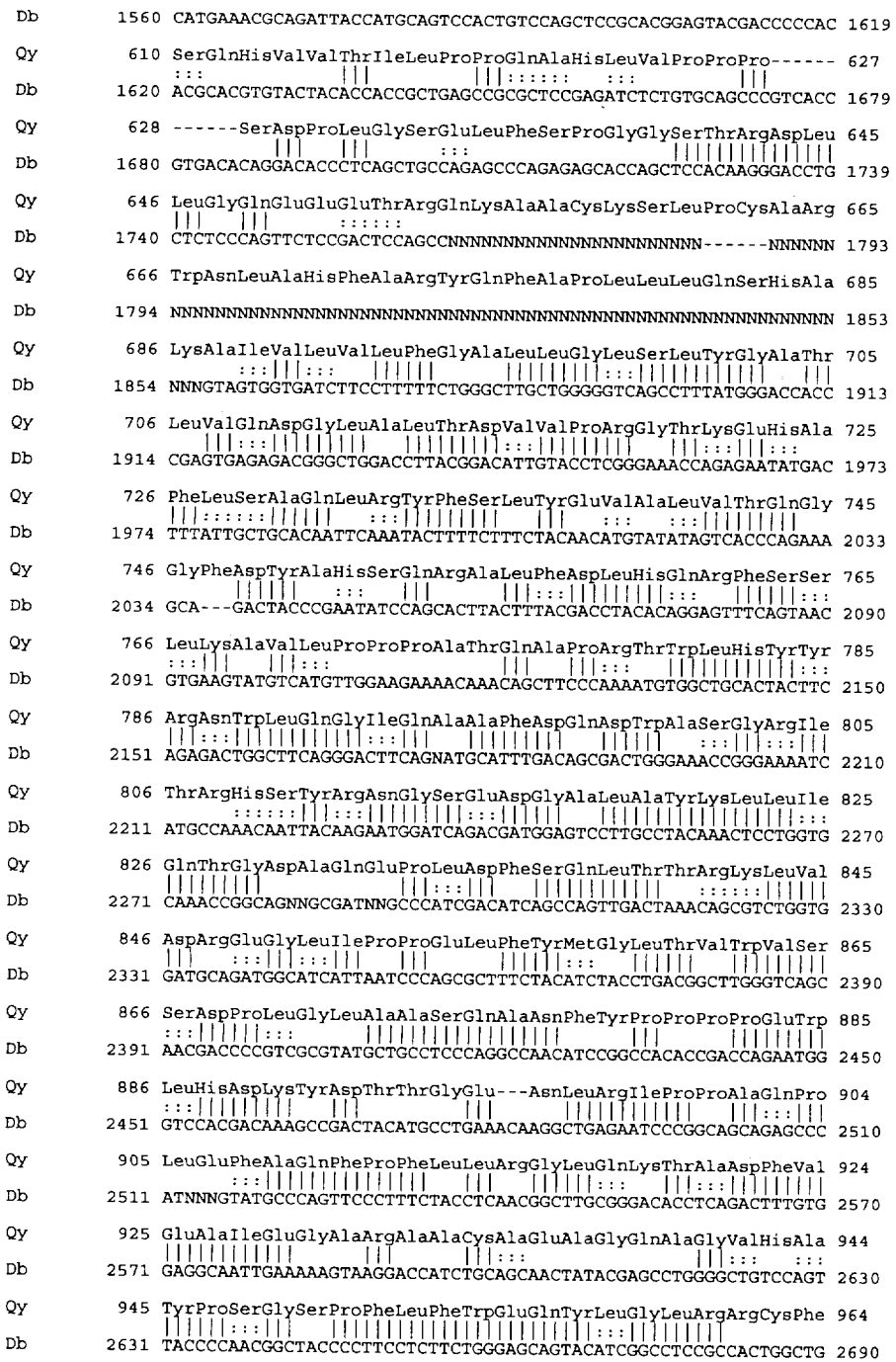
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 3950)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3950)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .3950
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>3950
/gene="PTCH"
/locus_tag="HCM5573"
ORIGIN

Alignment Scores:

Pred. No.:	3.44e-199	Length:	3950
Score:	2362.00	Matches:	515
Percent Similarity:	53.59%	Conservative:	164
Best Local Similarity:	40.65%	Mismatches:	402
Query Match:	37.66%	Indels:	186
DB:	9	Gaps:	17

US-09-990-046-2 (1-1203) x AY415486 (1-3950)

```
Qy        90 GlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAlaAla 109
Db         3 GGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCTATG 62

Qy       110 TyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrPro 129
Db        63 TTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACCACA 122

Qy       130 GluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeu 149
Db       123 GAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCACGTATACATG 182

Qy       150 TyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIleGlu 169
Db       183 TACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACAGAA 242

Qy       170 AsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrProLeu 189
Db       243 ACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCTTTG 302

Qy       190 AspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgPro 209
Db       303 GACTGCTTCTGGGAAGGGGCAAAATTACAGTCTGGGACAGCATACCTCCTNNNNNNNNNN 362

Qy       210 AspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPheAla 229
Db       363 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 422

Qy       230 SerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGly 249
Db       423 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 482

Qy       250 ArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHisHisSer 269
Db       483 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 542

Qy       270 ArgGlnAlaPro---AsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHis 288
Db       543 NNNNNNNNNCCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCCAGA 602

Qy       289 LysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGly 308
Db       603 AAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACTGGA 662

Qy       309 GluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeu 328
Db       663 AAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAAATG 722

Qy       329 TyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGluGln 347
Db       723 TACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGACAAA 779

Qy       348 AlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeu 367
Db       780 GCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGTGTC 839

Qy       368 ProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeu 387
Db       840 GCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATCCTG 899

Qy       388 HisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAla 407
Db       900 AAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGNNNNNN 959

Qy       408 TyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeu 427
Db       960 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1019

Qy       428 AlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeu 447
Db      1020 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1079

Qy       448 GlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGly 467
Db      1080 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTTGCCATTTCTCGCTCTTGGTGTTGGT 1139

Qy       468 ValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------Thr 485
Db      1140 GTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGAATC 1199

Qy       486 ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeuThr 505
Db      1200 CCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTCACG 1259

Qy       506 SerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArg 525
Db      1260 TCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCNNNTTCCCGCTCTGCGG 1319

Qy       526 AlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuVal 545
Db      1320 GCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTCATT 1379

Qy       546 PheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspValLeu 565
Db      1380 TTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATTTTC 1439

Qy       566 CysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGly 585
Db      1440 TGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTACACC 1499

Qy       586 Asp--------------------GlyThrValProValGlyIleAlaHis--------- 595
Db      1500 GACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTTGCC 1559

Qy       596 ------------------LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSer 609
```


Db 1560 CATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCCCAC 1619
Qy 610 SerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro------ 627
Db 1620 ACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTCACC 1679
Qy 628 ------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAspLeu 645
Db 1680 GTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGACCTG 1739
Qy 646 LeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArg 665
Db 1740 CTCTCCCAGTTCTCCGACTCCAGCCNNNNNNNNNNNNNNNNNNNNNN------NNNNNN 1793
Qy 666 TrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAla 685
Db 1794 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1853
Qy 686 LysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThr 705
Db 1854 NNNGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACC 1913
Qy 706 LeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAla 725
Db 1914 CGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATATGAC 1973
Qy 726 PheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGly 745
Db 1974 TTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAGAAA 2033
Qy 746 GlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSer 765
Db 2034 GCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGTAAC 2090
Qy 766 LeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyr 785
Db 2091 GTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTACTTC 2150
Qy 786 ArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIle 805
Db 2151 AGAGACTGGCTTCAGGGACTTCAGNATGCATTTGACAGCGACTGGGAAACCGGGAAAATC 2210
Qy 806 ThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIle 825
Db 2211 ATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTGGTG 2270
Qy 826 GlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVal 845
Db 2271 CAAACCGGCAGNNGCGATNNGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTGGTG 2330
Qy 846 AspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSer 865
Db 2331 GATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTCAGC 2390
Qy 866 SerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrp 885
Db 2391 AACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAATGG 2450
Qy 886 LeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPro 904
Db 2451 GTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAGCCC 2510
Qy 905 LeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheVal 924
Db 2511 ATNNNGTATGCCCAGTTCCCTTTCTACCTCAACGGCTTGCGGGACACCTCAGACTTTGTG 2570
Qy 925 GluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAla 944
Db 2571 GAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCCAGT 2630
Qy 945 TyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPhe 964
Db 2631 TACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGGCTG 2690
Qy 965 LeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeu 984
Db 2691 CTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTG 2750
Qy 985 AsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPhe 1004
Db 2751 AACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTC 2810
Qy 1005 GlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAla 1024
Db 2811 GGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATCGCT 2870
Qy 1025 SerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGln 1044
Db 2871 TCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCCATC 2930
Qy 1045 GlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAsp 1064
Db 2931 GGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTGGAC 2990
Qy 1065 GlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIle 1084
Db 2991 GGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTTGCGGGATCTGAGTTCGACTTCATT 3050
Qy 1085 Val---------- 1085
Db 3051 GTCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3110
Qy 1086 ---------ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHis 1102
Db 3111 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGTCTCCAGCCAAC 3170
Qy 1103 GlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluValIleGln 1122
Db 3171 GGCTTAAACCGCCTGCCCACA------CCCTCCCCTGAGCCACCCCCCAGCGTGGTCCGC 3224
Qy 1123 Met----------TyrLys 1125
Db 3225 TTCGCCATGCCGCCCGGCCACATGCACAGCGGCTCTGATTCCTCCGACTCGGAGTATAGT 3284
Qy 1126 Glu----------SerProGluIleLeuSerProProAlaProGlnGly 1138
Db 3285 TCCCAGACGACAGTGTCAGGCCTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGC 3344
Qy 1139 GlyGly---------- 1140
Db 3345 GCGGGAGGCCCTGCCCACCAAGTGATCGNNGAAGCCACAGAAAACCCCGNNTTCGCCCAC 3404
Qy 1140 ---------- 1140
Db 3405 TCCACTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3464
Qy 1140 ---------- 1140
Db 3465 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3524
Qy 1140 ---------- 1140
Db 3525 NNNNNNNNNNNNNNTGGCCACCCCNCTACAGACCGCGCAGAGACGCTTTTGAAATTNNN 3584
Qy 1141 ----------LeuArgTrpGly---------- 1144
Db 3585 NCTGAAGGGCATTCTGGCCCTAGCAATAGGGACCGCTGGGGCCCCTGCGGGGCCCGTTCT 3644
Qy 1145 ----------AlaSerSerSerLeuProGlnSerPheAla 1154
Db 3645 CACAACCCTCGGAACCCAGCGTCCACTGCCATGGGCAGCTCCGTGCCCGGCTACTGCCAG 3704
Qy 1155 ArgValThrThr----------SerMetThrValAlaIleHisProProProLeu 1169
Db 3705 CCCATCACCACTGTGACGGCTTCTGCCTCCGTGACTGTCGCCGTGCACCCGCCGCCTGTC 3764

```
Qy       1170 ProGlyAlaTyrIleHisPro 1176
              ||||||      :::|||
Db       3765 CCTGGGCCTGGGCGGAACCCC 3785

RESULT 4
CF733501
LOCUS       CF733501                711 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  UI-M-HB0-ckb-n-01-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
            IMAGE:30608088 5', mRNA sequence.
ACCESSION   CF733501
VERSION     CF733501.1  GI:37629834
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30608088"
                     /tissue_type="whole eye"
                     /dev_stage="embryo 12.5,13.5,14.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HB0"
                     /note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site .Double strand cDNA was
                     size selected according to mRNA size fraction ,ligated
                     with EcoR I adaptor , digested with NotI and then cloned
                     directionally into pYX-Asc vector . The library tag
                     sequence located between the Not I site and the polyA tail
                     is TTATTGAAGT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."
ORIGIN

Alignment Scores:
Pred. No.:              2.51e-87        Length:         711
Score:                  1097.50         Matches:        214
Percent Similarity:     91.14%          Conservative:   2
Best Local Similarity:  90.30%          Mismatches:     12
Query Match:            17.50%          Indels:         9
DB:                     7               Gaps:           1

US-09-990-046-2 (1-1203) x CF733501 (1-711)

Qy       178 GluLysLeuProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3 GAGAAGCTGTTTCCCTGTGTGATCCTCACCCCGCTTGACTGCTTCTGGGAAGGAGCCAAA 62

Qy       198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
```

```
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 CTCCAAGGGGGCTCTGCCTACTTGCCGGGCCGCCCTGATATCCAGTGGACCAACCTGGAC 122

Qy         218 ProGluGlnLeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeu 237
               |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 CCTCAGCAGCTGCTCGAGGAGCTGGGCCCCTTTGCCTCTCTGGAGGGCTTCCGGGAACTG 182

Qy         238 LeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAsp 257
               ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db         183 CTAGATAAGGCACAGGTGGGCCAGGCCTATGTGGGGCGACCCTGTCTGGACCCTGATGAC 242

Qy         258 LeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHis 277
               ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db         243 CCCCACTGTCCACCTAGTGCTCCCAACCGGCACAGCAGGCAGGCTCCCAATGTGGCTCAG 302

Qy         278 GluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeu 297
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 GAGCTGAGTGGGGGCTGCCATGGCTTCTCCCACAAGTTCATGCACTGGCAGGAGGAACTG 362

Qy         298 LeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArg--------------- 312
               ||||||||||||    |||||||||    |||||:::|||||||||
Db         363 CTACTAGGGGGCACAGCCAGAGATCTCCAAGGACAGCTGCTGAGGTCGGGCCTCCCCTGG 422

Qy         313 -------AlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGl 330
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         423 GACTTGGGCAGAGGCCTTGCAGAGCACCTTCCTGCTCATGAGTCCCCGTCAGCTGTACGA 482

Qy         330 uHisPheArgGlyAspTyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerTh 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         483 GCACTTCCGGGGGCGACTACCAGACACATGACATCGGCTGGAGCGAGGAGCAGGCCAGCAT 542

Qy         350 rValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAs 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||
Db         543 GGTGCTGCAGGCCTGGCAGAGGCGCTTTGTGCAGCTAGCCCAGGAGGCTCTGCCGGCCAA 602

Qy         370 nAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeu-AspAspIleLeuHisAlaP 390
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||    ||||
Db         603 CGCGTCNCAGCAGATCCATGCCTTCTCCTCCACCACCCTNGGATGACATCCTGCGCGCGT 662

Qy         390 heSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMet 405
               ||||||||||||||      |||||||||    ||||||||||||||
Db         663 TCTCTGAAGTCAGCACCACCCGTGTGGTANGAGGCTATCTGCTTATG 709

RESULT 5
CK830937
LOCUS       CK830937                708 bp    mRNA    linear   EST 04-MAR-2004
DEFINITION  4054508 BARC 8BOV Bos taurus cDNA clone 8BOV_18P22 5', mRNA
            sequence.
ACCESSION   CK830937
VERSION     CK830937.1  GI:45056596
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
  TITLE     Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt '' -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 18  row: P  column: 22
```

```
          Seq primer: CCTATTTAGGTGACACTATAGAAC
          High quality sequence stop: 708.
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="8BOV_18P22"
                     /sex="Female"
                     /tissue_type="Epithelial, Muscle"
                     /dev_stage="Lactating, Neonatal"
                     /lab_host="DH10B TonA"
                     /clone_lib="BARC 8BOV"
                     /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
                     NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
                     library in pCMVsport6.1, constructed from equimolar mRNA
                     pools derived from 5 sources, 4 lactating intestinal, 1
                     neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                     Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                     Duodenum, Jejunum, Distal Ileum"
ORIGIN

Alignment Scores:
Pred. No.:                5.83e-85      Length:          708
Score:                    1071.00       Matches:         212
Percent Similarity:       96.43%        Conservative:    4
Best Local Similarity:    94.64%        Mismatches:      8
Query Match:              17.08%        Indels:          0
DB:                       7             Gaps:            0

US-09-990-046-2 (1-1203) x CK830937 (1-708)

Qy        897 LeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGly 916
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         12 CTTCGCATCCCGGCGGCCCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTCCTGCGCGGC 71

Qy        917 LeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGlu 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 CTCCAGAAGACTGCAGACTTCGTGGAGGCCATTGAGGGGGCCCGGGCAGCGTGTGCTGAG 131

Qy        937 AlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGln 956
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GCCAGCCAGGCCGGGGTGCATGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAGCAG 191

Qy        957 TyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPhe 976
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db        192 TACCTGGGCCTGCGGCGCTGCTTCCTGCTGGCAGTCTGCATCCTGCTGCTGTGTACTTTC 251

Qy        977 LeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeu 996
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        252 CTCGTCTGTGCCCTGCTGCTGCTCAACCCCTGGACGGCTGCGCTCATAGTACTGGTCCTG 311

Qy        997 AlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAla 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GCGATGATGACTGTGGAGCTCTTTGGCATCATGGGTTTCCTGGGCATCAAGCTGAGTGCC 371

Qy       1017 IleProValValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisVal 1036
              |||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        372 ATCCCGGTGGTGATTCTTGTGGCCTCCATAGGCATCGGTGTCGAGTTCACCGTCCACGTG 431

Qy       1037 AlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGlu 1056
              ||||||||||||||||  ||||||||||||||||||||||||  |||||||||
Db        432 GCTCTGGGCTTCCTGACCGCTCAGGGTAGCCGGAACCTGCGGGCTGCCCGGGCCCTGGAG 491

Qy       1057 HisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeu 1076
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 CGCACATTTGCTCCAGTGACCGATGGGGCCATCTCCACGTTGCTAGGTCTGCTCATGCTT 551

Qy       1077 AlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThr 1096
              |||||||||:::|||||||||||||||||||||||||||||  ||||||:::||||||
Db        552 GCTGGCTCCAACTTTGACTTCATCGTAAGGTACTTCTTTGTGGTGCTGACAATACTTACA 611
```

```
Qy       1097 LeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyPro 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 CTCCTGGGCCTCCTCCATGGGCTCGTGCTGCTGCCGGTACTGCTGTCCATCCTGGGCCCC 671

Qy       1117 ProProGluVal 1120
              ||||||||||||
Db        672 CCACCAGAGGTG 683

RESULT 6
CF531700
LOCUS       CF531700                662 bp    mRNA    linear   EST 12-SEP-2003
DEFINITION  UI-M-FY0-cgq-d-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
            IMAGE:30356154 5', mRNA sequence.
ACCESSION   CF531700
VERSION     CF531700.1  GI:34583668
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .662
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30356154"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FY0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

Alignment Scores:
Pred. No.:                1.67e-82      Length:          662
Score:                    1043.00       Matches:         199
Percent Similarity:       94.09%        Conservative:    8
Best Local Similarity:    90.45%        Mismatches:      13
Query Match:              16.63%        Indels:          0
DB:                       7             Gaps:            0

US-09-990-046-2 (1-1203) x CF531700 (1-662)
```

```
Qy        593 IleAlaHisLeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSerGlnHis 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ATTGCCCACCTGACTGCCACCGTGCAAGCCTTCACCCACTGCGAAGCCAGCAGCCAGCAT 61

Qy        613 ValValThrIleLeuProProGlnAlaHisLeuValProProProSerAspProLeuGly 632
              ||||||||||||||||||||||||||||||||||:::   |||   ||||||||||||||||
Db         62 GTAGTCACCATTTTGCCTCCTCAAGCCCACCTGCTGTCTCCAGCTTCTGACCCACTGGGC 121

Qy        633 SerGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThr 652
              |||||||||:::|||||||||||||||||||||||||||||   |||||||||   |||
Db        122 TCCGAACTCTATAGCCCTGGAGGGTCTACACGGGACCTTCTCAGTCAGGAGGAGGGGACA 181

Qy        653 ArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAla 672
                    :::||||||||||:::   |||   ||||||   |||   ||||||||||||||||
Db        182 GGGCCACAGGCGGCCTGCAGGCCCCTGCTCTGTGCCCACTGGACTCTCGCCCATTTTGCC 241

Qy        673 ArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeu 692
              ||||||||||||||||||||||||||||||:::   |||||||||:::||||||:::
Db        242 CGCTATCAGTTTGCACCTTTACTGCTCCAGACACGAGCCAAGGCCCTGGTGTTGCTGTTC 301

Qy        693 PheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAla 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TTTGGGGCTCTTTTGGGCCTGAGCCTCTATGGAGCCACCTTGGTACAAGATGGGCTGGCC 361

Qy        713 LeuThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArg 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGACAGATGTGGTCCCTAGGGGCACCAAGGAACATGCTTTCCTGAGCGCCCAGCTCAGG 421

Qy        733 TyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSer 752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TACTTCTCCCTGTACGAGGTGGCTCTAGTGACACAGGGTGGCTTTGACTACGCCCACTCC 481

Qy        753 GlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGCTCCCTCAAGGCTGTGCTGCCCCCA 541

Qy        773 ProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIle 792
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        542 CCTGCCACCCAGGCACCCCGCACCTGGCTTCACTACTACCGCAGCTGGCTACAGGGTATC 601

Qy        793 GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsn 812
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        602 CAGGCTGCATTTGACCAAGACTGGGCTTCTGGGCGCATCACCTGCCACTCTTACCGCAAC 661
```

RESULT 7
CN671167

```
LOCUS       CN671167                603 bp    mRNA    linear   EST 17-MAY-2004
DEFINITION  A0902E10-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high
            density) cDNA library (Long) Mus musculus cDNA clone NIA:A0902E10
            IMAGE:30767001 5', mRNA sequence.
ACCESSION   CN671167
VERSION     CN671167.1  GI:47437618
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
  TITLE     Transcriptome analysis of mouse stem cells and early embryos
  JOURNAL   PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: A0902  row: E  column: 10
            Seq primer: M13 Reverse
            High quality sequence stop: 603
            POLYA=No.
FEATURES    Location/Qualifiers
     source 1. .603
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="129Sv/EvTac"
            /db_xref="niaEST:A0902E10-5"
            /db_xref="taxon:10090"
            /clone="NIA:A0902E10 IMAGE:30767001"
            /sex="Male"
            /tissue_type="Embryonic Stem Cell"
            /cell_line="129.3 ES cells"
            /lab_host="DH10B"
            /clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48
            h, high density) cDNA library (Long)"
            /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
            Site_2: NotI; Mouse cDNA project by the Laboratory of
            Genetics, National Institute on Aging (NIA), Intramural
            Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
            This is a long-transcript enriched cDNA library (Ref.
            Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
            cells were plated at density 3x104/cm2, on gelatin-coated
            plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
            medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
            0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
            beta-mercaptoethanol, 1000 U/ml LIF, 100 U/ml penicillin,
            and 100 ug/ml streptomycin. Double-stranded cDNAs were
            synthesized with an Oligo(dT) primer [Invitrogen:
            5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT-3'] from
            2ug of total RNA, treated with T4 DNA polymerase, and
            purified by ethanol-precipitation. The cDNAs were ligated
            to Lone-linker LL-Sal4, purified by phenol/chloroform, and
            separated from free linkers by Centricon 100. Then, the
            cDNAs were amplified by long-range high fidelity PCR using
            Ex Taq polymerase (Takara) with a primer Sal4-S. The
            products were purified by phenol/chloroform and Centricon
            100. The cDNAs were digested with SalI and NotI enzymes
            and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
            vector. The DH10B E. coli host was transformed with the
            ligation mixture by the standard chemical method. The
            average insert size is about 2.7 kb. The library was
            constructed by Yulan Piao."
ORIGIN
```

Alignment Scores:

Pred. No.:	1.38e-81	Length:	603
Score:	1032.00	Matches:	190
Percent Similarity:	96.00%	Conservative:	2
Best Local Similarity:	95.00%	Mismatches:	8
Query Match:	16.45%	Indels:	0
DB:	7	Gaps:	0

US-09-990-046-2 (1-1203) x CN671167 (1-603)

```
Qy        156 LeuAsnLysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrp 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 TTGAACAAGATCTGCTACAAATCAGGGGTTCCCCTTATTGAAAATGGGATGATCGAGCGG 62

Qy        176 MetIleGluLysLeuProCysValIleLeuThrProLeuAspCysPheTrpGluGly 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGATTGAGAAGCTGTTTCCCTGTGTGATCCTCACCCCGCTTGACTGCTTCTGGGAAGGA 122

Qy        196 AlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsn 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCCAAACTCCAAGGGGGCTCTGCCTACTTGCCGGGCCGCCCTGATATCCAGTGGACCAAC 182

Qy        216 LeuAspProGluGlnLeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArg 235
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CTGGACCCTCAGCAGCTGCTCGAGGAGCTGGGCCCCTTTGCCTCTCTGGAGGGCTTCCGG 242
```

```
Qy        236 GluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisPro 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        243 GAACTGCTAGATAAGGCACAGGTGGGCCAGGCCTATGTGGGGCGACCCTGTCTGGACCCT 302

Qy        256 AspAspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnVal 275
              |||||   |||||||||||||||||||||||    |||||||||||||||||||||||
Db        303 GATGACCCCCACTGTCCACCTAGTGCTCCCAACCGGCACAGCAGGCAGGCTCCCAATGTG 362

Qy        276 AlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu 295
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCTCAGGAGCTGAGTGGGGGCTGCCATGGCTTCTCCCACAAGTTCATGCACTGGCAGGAG 422

Qy        296 GluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAla 315
              ||||||||||||||||||    |||||||||   |||||:::||||||||||||||||||
Db        423 GAACTGCTACTAGGGGGCACAGCCAGAGATCTCCAAGGACAGCTGCTGAGGGCAGAGGCC 482

Qy        316 LeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAsp 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TTGCAGAGCACCTTCCTGCTCATGAGTCCCCGTCAGCTGTACGAGCACTTCCGGGGCGAC 542

Qy        336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        543 TACCAGACACATGACATCGGCTGGAGCGAGGAGCAGGCCAGCATGGTGCTGCAGGCCTGG 602
```

```
RESULT 8
BM105989
LOCUS       BM105989                571 bp    mRNA    linear   EST 21-NOV-2001
DEFINITION  509593 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM105989
VERSION     BM105989.1  GI:17037059
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 102  row: B  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..571
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 3BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from marrow, alveolar
                     macrophage, ovary, fetal semitendonosus muscle, and fetal
                     longissimus muscle."
ORIGIN

Alignment Scores:
Pred. No.:              3.29e-79        Length:         571
Score:                  1005.00         Matches:        184
Percent Similarity:     98.95%          Conservative:   4
Best Local Similarity:  96.84%          Mismatches:     2
Query Match:            16.02%          Indels:         0
DB:                     4               Gaps:           0

US-09-990-046-2 (1-1203) x BM105989 (1-571)
```

```
Qy        770 LeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeu 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db          1 CTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTACTACCGCAGCTGGCTA 60

Qy        790 GlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSer 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGGAATCCAGGCTGCATTTGACCAGGACTGGGCTTCTGGGCGCATCACCCGCCACTCA 120

Qy        810 TyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAsp 829
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        121 TACCGCAATGGCTCTGAGGATGGGGCCCTGGCATACAAGCTGCTCGTCCAGACCGGGGAT 180

Qy        830 AlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGly 849
              |||||||||||||||||||||||||||||||:::||||||||||||:::||||||
Db        181 GCCCAGGAGCCTCTAGATTTCAGCCAGCTGACCACCAAGAAGCTGGTGGACAAGGAAGGG 240

Qy        850 LeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeu 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATCCCACCCGAGCTCTTCTACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTG 300

Qy        870 GlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLys 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTCTGGCAGCCTCACAGGCCAACTTCTATCCCCCACCTCCTGAGTGGCTGCATGACAAG 360

Qy        890 TyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAlaGln 909
              ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db        361 TATGACACCACGGGGGAGAATCTTCGCATCCCGGCGGCCCAGCCCTTGGAGTTTGCCCAG 420

Qy        910 PheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGly 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCCCCTTCCTCCTGCGCGGCCTCCAGAAGACTGCAGACTTCGTGGAGGCCATTGAGGGG 480

Qy        930 AlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySer 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGGGCAGCGTGTGCTGAGGCCAGCCAGGCCGGGGTGCATGCCTACCCCAGCGGCTCC 540

Qy        950 ProPheLeuPheTrpGluGlnTyrLeuGly 959
              ||||||||||||||||||||||||||||||
Db        541 CCCTTCCTCTTCTGGGAGCAGTACCTGGGC 570
```

```
RESULT 9
CA528868
LOCUS       CA528868                600 bp    mRNA    linear   EST 15-NOV-2002
DEFINITION  8091-13 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
ACCESSION   CA528868
VERSION     CA528868.1  GI:25042932
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
  TITLE     Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
  JOURNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
  MEDLINE   21671825
   PUBMED   11812828
COMMENT     Contact: Klein WH
```

Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES Location/Qualifiers
source 1. .600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Alignment Scores:

Pred. No.:	1.5e-78	Length:	600
Score:	998.00	Matches:	190
Percent Similarity:	97.49%	Conservative:	4
Best Local Similarity:	95.48%	Mismatches:	5
Query Match:	15.91%	Indels:	0
DB:	6	Gaps:	0

US-09-990-046-2 (1-1203) x CA528868 (1-600)

```
Qy        829 AspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGlu 848
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db          3 AATGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACCACAAGGAAACTGGTGGACAAGGAG 62

Qy        849 GlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspPro 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GGACTCATTCCCCCAGAGCTCTTCTACATGGGGCTAACCGTGTGGGTGAGCAGCGACCCC 122

Qy        869 LeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAsp 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CTGGGCCTCGCAGCCTCTCAGGCCAACTTCTACCCCCCACCTCCAGAGTGGCTTCACGAC 182

Qy        889 LysTyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAla 908
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        183 AAATATGATACCACCGGGGAGAACCTTCGCATCCCGGCAGCCCAGCCCTTGGAGTTTGCC 242

Qy        909 GlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGlu 928
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        243 CAGTTCCCCTTCCTGCTGCATGGACTCCAGAAGACTGCAGACTTTGTAGAAGCCATCGAA 302

Qy        929 GlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGly 948
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        303 GGGGCCAGGGCGGCATGCACAGAGGCAGGCCAGGCAGGGGTGCATGCCTACCCCAGTGGC 362

Qy        949 SerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaVal 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TCCCCCTTCCTCTTCTGGGAGCAGTATCTGGGTCTTCGGCGCTGCTTCCTGCTGGCAGTC 422

Qy        969 CysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThr 988
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        423 TGCATCTTGCTGGTGTGCACCTTCCTCGTCTGTGCCCTGCTTCTACTCAGCCCGTGGACA 482

Qy        989 AlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGly 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GCTGGCCTCATAGTGCTGGTCCTGGCAATGATGACTGTGGAGCTCTTTGGTATCATGGGA 542

Qy       1009 PheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSerValGly 1027
              ||||||||||||||||||||||||||||||  ||||||  |||||||:::|||
Db        543 TTCCTGGGCATCAAACTGAGTGCCATCCCCGTGGNAATCCTCGNGGCCTCTATAGGC 599
```

RESULT 10
CN676164
LOCUS CN676164 625 bp mRNA linear EST 17-MAY-2004
DEFINITION A0976A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0976A07 IMAGE:30774054 5', mRNA sequence.
ACCESSION CN676164
VERSION CN676164.1 GI:47442615
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 625)
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE Transcriptome analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0976 row: A column: 07
Seq primer: M13 Reverse
High quality sequence stop: 625
POLYA=No.
FEATURES Location/Qualifiers
source 1. .625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:A0976A07-5"
/db_xref="taxon:10090"
/clone="NIA:A0976A07 IMAGE:30774054"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES cells were plated at density 3x104/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 1000 U/ml LIF, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:

Pred. No.:	1.26e-77	Length:	625
Score:	988.00	Matches:	194
Percent Similarity:	96.63%	Conservative:	7
Best Local Similarity:	93.27%	Mismatches:	7

```
Query Match:          15.75%      Indels:        0
DB:                   7           Gaps:          0

US-09-990-046-2 (1-1203) x CN676164 (1-625)

Qy        910 ProProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGly 929
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTCCCCTTCCTGCTGCATGGACTCCAGAAGACTGCAGACTTTGTAGAAGCCATCGAAGGG 61

Qy        930 AlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySer 949
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCCAGGGCGGCATGCACAGAGGCAGGCCAGGCAGGGGTGCATGCCTACCCCAGTGGCTCC 121

Qy        950 ProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCys 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCCTTCCTCTTCTGGGAGCAGTATCTGGGTCTTCGGCGCTGCTTCCTGCTGGCAGTCTGC 181

Qy        970 IleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAla 989
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        182 ATCTTGCTGGTGTGCACCTTCCTCGTCTGTGCCCTGCTTCTACTCAGCCCGTGGACAGCT 241

Qy        990 GlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPhe 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGCCTCATAGTGCTGGTCCTGGCAATGATGACTGTGGAGCTCTTTGGTATCATGGGATTC 301

Qy       1010 LeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGly 1029
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        302 CTGGGCATCAAACTGAGTGCCATCCCCGTGGTAATCCTCGTGGCCTCTATAGGCATTGGT 361

Qy       1030 ValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeu 1049
              ||||||||||||||||||||||||||||||||||||:::   ||||||||||||||||||||
Db        362 GTTGAATTCACAGTTCACGTGGCTCTGGGCTTCCTGACCAGCCATGGTAGCCGGAACCTG 421

Qy       1050 ArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThr 1069
              ||||||||   |||||||||  ||||||||||||||||||||||:::||||||||||||||
Db        422 CGGGCTGCTAGCGCTCTGGAACAGACCTTTGCCCCTGTGACTGATGGAGCTGTCTCCACC 481

Qy       1070 LeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePhe 1089
              ||||||||||||||||||||||||||||||:::||||||||||||:::||||||||||||||
Db        482 TTGCTGGGTCTGCTCATGCTTGCTGGTTCTAACTTTGACTTCATCATAAGGTATTTCTTT 541

Qy       1090 AlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProVal 1109
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        542 GTGGTGCTGACGGTGCTGACACTCTTGGGCCTGCTCCATGGACTCCTGCTGCTGCCTGTG 601

Qy       1110 LeuLeuSerIleLeuGlyProPro 1117
              |||||||||||||||||||||||
Db        602 CTGCTCTCTATCCTAGGCCCCCCG 625

RESULT 11
BX844270
LOCUS       BX844270                911 bp    mRNA    linear   EST 11-DEC-2003
DEFINITION  BX844270 NICHD_XGC_Emb3 Xenopus laevis cDNA clone IMAGp998A148295 ;
            IMAGE:3399061 5', mRNA sequence.
ACCESSION   BX844270
VERSION     BX844270.1  GI:39734371
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D.,
            Schroth,A., Korn,B. and Landgrebe,J.
  TITLE     Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998A148295.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
            No.998) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
            laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            SP6, 5' ATTTAGGTGACACTATAG 3'.
FEATURES              Location/Qualifiers
     source           1. .911
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="IMAGp998A148295 ; IMAGE:3399061"
                      /tissue_type="embryo (stages 24-25)"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NICHD_XGC_Emb3"
                      /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                      Cloned unidirectionally. Primer: Oligo dT. Average insert
                      size 1.7 kb. Constructed by Life Technologies. Note: This
                      is a Xenopus Gene Collection (XGC) library."
ORIGIN

Alignment Scores:
Pred. No.:                9.38e-76      Length:          911
Score:                    970.00        Matches:         192
Percent Similarity:       75.00%        Conservative:    27
Best Local Similarity:    65.75%        Mismatches:      37
Query Match:              15.47%        Indels:          36
DB:                       5             Gaps:            4

US-09-990-046-2 (1-1203) x BX844270 (1-911)

Qy          2 ThrArgSerPro---------------ProLeuArgGluLeuProPro------------ 12
              |||   ||||||                |||:::      :::||||||
Db         28 ACCCCCTCTCCTGCCTGCTGTAGGATACCGATGGCCTCTGTTCCCCCCTGTGCGGGGGAG 87

Qy         13 ---------SerTyrThrProPro---------------------------------- 17
                      ::::::   ||||||
Db         88 AGGGGCTTTACACATCTCCCCCCGGGTTACAAAAGCAAACAGCCTGCTCCCAGCTCGGAT 147

Qy         18 --------------------------AlaArgThrAlaAlaProGlnIleLeuAlaGly 28
                                         |||   |||      ||||||     |||
Db        148 CTACTGAGGAGACCCAGCTATTGCCATGCCGCCTTTGCACTCAAGCAGATCGCTAAGGGT 207

Qy         29 SerLeu---------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPhe 45
                            ||||||||||||||||||||||||   ||||||   |||||||||
Db        208 AAGGCTGTTGGCCAAAAGGCTCCTCTCTGGCTACGAGCTCAGTTCCAAGCCTTGCTCTTC 267

Qy         46 SerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAla 65
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||
Db        268 ATCCTGGGCTGCTCCATCCAGAGACACTGCGGGAAGGTCTTGTTCATTGGATTGCTGGTG 327

Qy         66 PheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeu 85
              ||||||||||||||:::|||||||||:::|||  ||||||||:::::|||:::|||
Db        328 TTTGGGGCTCTTGCTGTGGGCCTTCGTGTGGCTTCCATTGAGACTGATATCGAAAGGTTG 387

Qy         86 TrpValGluValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGly 105
              |||||||||   ||||||||||||||   ||||||   ||||||||||||||||||||
Db        388 TGGGTGGAAGCTGGAAGCAGAGTGAGCCATGAGCTTCGCTACACTAAGGAGAAATTGGGA 447

Qy        106 GluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsn 125
              ||||||:::   ||||||||||||||||||||||||||   ::::::||||||   |||
Db        448 GAAGAATCTGTATATACCTCACAAATGCTGATCCAGACACCTAAAAGGGAAGGAGGAAAT 507

Qy        126 IleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysVal 145
              |||||||||   |||||||||  ||||||||||:||||||||   ||||||||||||
Db        508 ATACTGACCAATGAAGCCTTGCTTCTTCATCTGAGAGCAGCTCTTGCTGCAAGTAAAGTT 567

Qy        146 GlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyVal 165
```

```
Db        568 CAAGTGTCTATGTATGGAAAATCTTGGGACCTGAATCAAATCTGTTATAAATCTGGAGTT 627

Qy        166 ProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIle 185

Db        628 CCAATTATTGAAAATGGCATGATTGAGAGGATGATTGAGAAACTTTTCCCTTGTGTAATA 687

Qy        186 LeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeu 205

Db        688 ATTACACCTCTGGACTGTTTTTGGGAAGGATCCCAGCTTCAAGGTGGCTCTGCATATCTA 747

Qy        206 ProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeu 225

Db        748 CCAGGAAGAGCTGACATTCAATGGACCAACCTAGATCCCATCAAGTTCATGGAAGAGCTT 807

Qy        226 GlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGln 245

Db        808 GGTCAGTTCACCAGTCTTGATGGCTTCAAGGAAATGCTGGACAAGGCTGAAGTAGGACAG 867

Qy        246 AlaTyrValGlyArgProCysLeuHisProAspAsp 257

Db        868 GGATATATGGAACGACCTTGTCTGGACCCTACAGAC 903
```

RESULT 12
BQ964086

```
LOCUS       BQ964086                974 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_10054944 NIH_MGC_134 Mus musculus cDNA clone
            IMAGE:6509228 5', mRNA sequence.
ACCESSION   BQ964086
VERSION     BQ964086.1  GI:22379564
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14076  row: c  column: 21
            High quality sequence stop: 689.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6509228"
                     /tissue_type="undifferentiated limb"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_134"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
                     this is a NIH_MGC Library."
ORIGIN
```

Alignment Scores:

Pred. No.:	1.01e-74	Length:	974
Score:	959.00	Matches:	199
Percent Similarity:	67.05%	Conservative:	35
Best Local Similarity:	57.02%	Mismatches:	76
Query Match:	15.29%	Indels:	39
DB:	5	Gaps:	4

US-09-990-046-2 (1-1203) x BQ964086 (1-974)

```
Qy        848 GluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAsp 867

Db         28 GATGGCATCATTAATCCGAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGAC 87

Qy        868 ProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeuHis 887

Db         88 CCTGTAGCTTACGCTGCCTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCAT 147

Qy        888 AspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGlu 906

Db        148 GACAAAGCCGACTACATGCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAG 207

Qy        907 PheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAla 926

Db        208 TACGCTCAGTTCCCTTTCTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCC 267

Qy        927 IleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrPro 946

Db        268 ATAGAAAAAGTGAGAGTCATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCC 327

Qy        947 SerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeu 966

Db        328 AATGGCTACCCCTTCCTGTTCTGGGAGCAGTACATCAGCCTGCGCCACTGGCTGCTGCTA 387

Qy        967 AlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnPro 986

Db        388 TCCATCAGCGTGGTGCTGGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCTGAACCCC 447

Qy        987 TrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIle 1006

Db        448 TGGACGGCCGGGATCATTGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATG 507

Qy       1007 MetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSerVal 1026

Db        508 ATGGGCCTCATCGGGATCAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGCATCTGTT 567

Qy       1027 GlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySer 1046

Db        568 GGCATCGGAGTGGAGTTCACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCATTGGGGAC 627

Qy       1047 ArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGlyAla 1066

Db        628 AAGAACCACAGGGCTATGCTCGCTCTGGAGCACATGTTTGCTCCCGTTCTGGACGGTGCT 687

Qy       1067 IleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArg 1086

Db        688 GTGTCCACTCTGCTGGGTGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTCAGA 747

Qy       1087 TyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeu 1106

Db        748 TACTTCTTTGCCGTCCTGGCCATTCTCACCGTCTTGGGGGTTCTCAATGGACTGGTTCTG 807

Qy       1107 LeuProValLeuLeuSerIleLeuGlyProProProGluValIleGlnMetTyrLysGlu 1126

Db        808 CTGCCTGTCCTCTTATCCTTCTTTGGACCGGGTCCC---------------------- 843

Qy       1127 SerProGluIleLeuSerProProAlaProGlnGlyGlyGlyLeuArgTrpGlyAlaSer 1146

Db        844 ----------------------------------------------------TGAGGGGTCTCC 855

Qy       1147 SerSerLeuProGlnSerPheAlaArgValThrThrSerMetThrValAlaIleHis-Pr 1166

Db        856 AGCCAATGGCCTAAACCGACTGCC----------------------------CACTCC 885

Qy       1166 oProProLeuProGlyAlaTyrIleHisProAlaProAspGluProProTrpSerPro-- 1185

Db        886 TTCGCCTGAGCCGCCCCCCAGGGGTCGTCCGGGTTTGGCGGTGCCCTCCTGGTCACCGGA 945

Qy       1186 -------AlaAlaThrSerSerGly 1191

Db        946 AAAAAGGGNTCGGATTTCTTCCGGA 970
```

RESULT 13
BB612664
LOCUS BB612664 639 bp mRNA linear EST 26-OCT-2001
DEFINITION BB612664 RIKEN full-length enriched, 10 day neonate skin Mus musculus cDNA clone 4731420O17 5', mRNA sequence.
ACCESSION BB612664
VERSION BB612664.1 GI:16453542
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 639)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
FEATURES Location/Qualifiers
source 1. .639
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4731420O17"
/sex="mixed"
/tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 day neonate skin"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Alignment Scores:

Pred. No.:	3.44e-70	Length:	639
Score:	905.00	Matches:	179
Percent Similarity:	91.43%	Conservative:	13
Best Local Similarity:	85.24%	Mismatches:	18
Query Match:	14.43%	Indels:	1
DB:	2	Gaps:	0

US-09-990-046-2 (1-1203) x BB612664 (1-639)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              |||   |||           |||   |||||||||||||||||||||||||||||||:::
Db         10 ATGGTTCGGCCACTGTCCCTTGGAGAGCTACCTCCCAGCTACACACCTCCAGCTCGGTCC 69

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              :::||||||   |||||||||||||||||||:::|||||||||||||||||||||||||||
Db         70 TCCGCACCTCATATCCTAGCTGGGAGCCTGCAGGCTCCTCTCTGGCTTCGAGCTTACTTC 129

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||   ||||||:::|||||||||||||||||||||
Db        130 CAAGGTCTACTCTTCTCCCTGGGGTGCAGGATCCAGAAACACTGCGGCAAAGTGCTCTTC 189

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              |||||||||:::|||||||||||||||||||||||||||||||:::|||:::||||||||||
Db        190 CTGGGACTGGTGGCCTTTGGGGCTCTGGCACTGGGTCTCCGAGTGGCTGTAATTGAGACA 249

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCTAGAACAGCTCTGGGTAGAAGTGGGCAGCAGGGTGAGCCAGGAGCTGCACTACACC 309

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 AAGGAGAAGCTGGGGGAAGAGGCTGCGTACACCTCCCAGATGTTGATTCAGACTGCGCAC 369

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              |||||||||   |||:::|||||||||||||||||||   ||||||||||||||||||||
Db        370 CAGGAAGGGGGAAACGTCCTCACCCCCGAGGCACTTGACTTGCACCTCCAGGCGGCGCTC 429

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAATCCTGGGATTTGAACAAGATCTGC 489

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||   |||||||||||||||||||||||||:::   ||||||:::||||||
Db        490 TACAAATCACGGGTTCCTCTTATTGAAAATGGGATGATCCAGCGGATGATTGACAAACTG 549

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              |||||||||||||||||||||||||||||||||||:::   |||:::||||||
Db        550 TCTTCCTGTGTGATCCTCACCCCGCTTGACTGCTTCTGGGATGA-GCCCAACTCCAATGG 608

Qy        201 GlySerAlaTyrLeuProGlyArgProAsp 210
              ||||||   ||||||||||   ||||||
Db        609 GGCTCTGTCTACTTGCCCGGCCCGCCTGAT 638
```

RESULT 14
BE234509
LOCUS BE234509 573 bp mRNA linear EST 10-JUL-2000
DEFINITION 141639 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.

```
ACCESSION   BE234509
VERSION     BE234509.1  GI:9019227
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 79  row: O  column: 17
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 1PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
ORIGIN

Alignment Scores:
Pred. No.:                5.15e-69        Length:          573
Score:                    891.00          Matches:         173
Percent Similarity:       92.67%          Conservative:    4
Best Local Similarity:    90.58%          Mismatches:      14
Query Match:              14.21%          Indels:          0
DB:                       2               Gaps:            0

US-09-990-046-2 (1-1203) x BE234509 (1-573)

Qy        502 ValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIle 521
              |||   ||||||||||||||||||||||    ||||||   ||||||||||||||||||||
Db          1 GTCGCGCTCACGTCCATCAACAACATGGTGGCCTTCTTCATGGCCGCCCTCGTGCCCATC 60

Qy        522 ProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAla 541
              |||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db         61 CCTGCCCTGCGGGCCTTCTCCTTGCAGGCGGCCATAGTGGTCGGCTGCAACTTCGCAGCC 120

Qy        542 ValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArg 561
              ||||||||||||||||||||:::|||||||||||||||   |||||||||||||||||
Db        121 GTGATGCTTGTCTTCCCGGCCGTCCTCAGCCTGGACCTGCACCGGCGCCACTGCCAGCGC 180

Qy        562 LeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuPro 581
              ||||||||||||||||||||:::|||||||||||||||:::|||||||||||||||||||
Db        181 CTTGATGTGCTCTGCTGCTTCGCAAGCCCCTGCTCTGCTCGGGTGATTCAGATTCTGCCC 240

Qy        582 GlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGln 601
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        241 CAGGAGCTGGGGGATGGGACAGTACCCGTGGGCATTGCCCGCTTGACTGCCACCGTTCAA 300

Qy        602 AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAla 621
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCTTTGCCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAACC 360

Qy        622 HisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySer 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACCTGGTGCCCCCACCTTCTGACCCTCTGGGCTCTGAGCTCTTCAGCCCGGGAGGGTCC 420

Qy        642 ThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeu 661
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        421 ACACGGGACCTTCTAGGCCAGGAGGAGGGGACACGGCAGAAGGCAGCCTGCAAGTCCCTG 480

Qy        662 ProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeu 681
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db        481 TCCTGTGCCCACTGGAATCTTGCCCATTTCGCCCGCTCTCAGTTTGCACCCTTGCTGCTC 540

Qy        682 GlnSerHisAlaLysAlaIleValLeuValLeu 692
              |||   ||||||||||||:::||||||||||||
Db        541 CAACCCCATGCCAAGGCCATGGTGCTGGTACTT 573

RESULT 15
CK639185
LOCUS       CK639185                 778 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  UI-M-HO0-cnx-o-06-0-UI.r1 NIH_BMAP_HO0 Mus musculus cDNA clone
            IMAGE:30638069 5', mRNA sequence.
ACCESSION   CK639185
VERSION     CK639185.1  GI:41365051
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30638069"
                     /tissue_type="Upper Head"
                     /dev_stage="9.5-10.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HO0"
                     /note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CGAACTGAAT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."
ORIGIN
```

Alignment Scores:

Pred. No.:	3.56e-68	Length:	778
Score:	884.00	Matches:	165
Percent Similarity:	83.72%	Conservative:	51
Best Local Similarity:	63.95%	Mismatches:	38
Query Match:	14.09%	Indels:	4
DB:	7	Gaps:	3

US-09-990-046-2 (1-1203) x CK639185 (1-778)

```
Qy        279 LeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeu 298
              |||:::|||||||||   |||   |||   |||:::|||||||||||||||||||||:::
Db          7 TTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAGTTGATT 66

Qy        299 LeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSer 318
              :::||||||      ::::::      |||:::|||:::   |||   |||||||||:::
Db         67 GTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTGCAAACC 126

Qy        319 ThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---AspTyrGln 337
                 |||   ||||||:::|||:::|||:::||||||||||||||||||   ||||||
Db        127 ATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGACTATGTC 186

Qy        338 ThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArg 357
              :::|||   |||   |||:::|||::::::|||:::   :::|||:::||||||||||||
Db        187 TCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGGCAGAGG 243

Qy        358 ArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAla 377
              :::|||::::::      :::::::::      |||::::::|||::::::
Db        244 ACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTTCTTCCC 303

Qy        378 PheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArg 397
              |||::::::||||||||||||||||||||||   :::||||||:::||||||     |||
Db        304 TTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTCATCCGA 363

Qy        398 ValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAsp 417
              |||      ||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        364 GTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGCTGGGAC 423

Qy        418 CysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaVal 437
              |||::::::|||||||||:::|||||||||||||||||||||||||||||||||:::|||
Db        424 TGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTGTCAGTG 483

Qy        438 AlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGln 457
              |||:::|||||||||||||||:::|||:::||||||:::||||||||||||||||||||
Db        484 GCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACAACTCAG 543

Qy        458 ValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAla 477
              |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        544 GTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCCCATGCA 603

Qy        478 PheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGluCysLeu 495
              |||:::|||                  |||   ::::::|||   ||||||||||||
Db        604 TTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAGTGCCTC 663

Qy        496 GlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMet 515
              :::|||||||||   ||||||   ||||||||||||:::|||:::   ||||||   |||
Db        664 AAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTCTTCATG 723

Qy        516 AlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
                  ||||||:::||||||||||||||||||||||||||||||||||||||:::
Db        724 GNCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 777
```

Search completed: November 22, 2004, 12:06:09
Job time : 5506 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 22, 2004, 07:43:25 ; Search time 25 Seconds
(without alignments)
4629.951 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

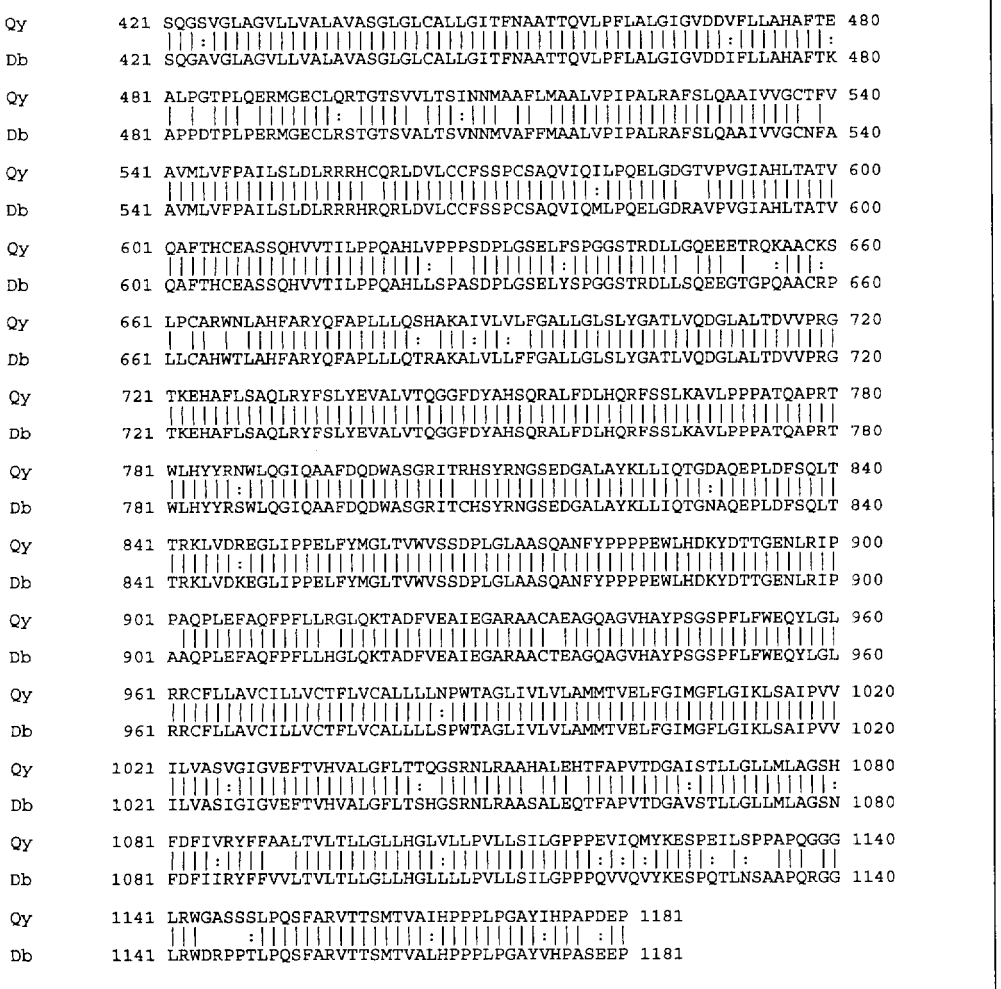
Result No.	Score	% Query Match	Length	DB	ID	Description
1	5599	89.3	1182	2	T13952	membrane protein p
2	4042.5	64.5	1220	2	T18291	patched protein -
3	3340	53.3	1442	2	T18538	patched protein -
4	3337	53.2	1434	2	T30172	transmembrane prot
5	1961.5	31.3	1299	1	S06119	membrane protein p
6	1708.5	27.2	1405	2	T27969	hypothetical prote
7	992	15.8	714	2	T16126	hypothetical prote
8	602.5	9.6	1278	2	T30188	Niemann-Pick C dis
9	514	8.2	1055	2	T05663	hypothetical prote
10	465.5	7.4	955	2	T21612	hypothetical prote
11	444	7.1	933	2	T25600	hypothetical prote
12	444	7.1	1003	2	T26746	hypothetical prote
13	430.5	6.9	1015	2	T15830	hypothetical prote
14	416.5	6.6	889	2	T29590	hypothetical prote
15	389.5	6.2	936	2	T26521	hypothetical prote
16	386.5	6.2	956	2	A89153	protein C24B5.3 [i
17	380.5	6.1	1170	2	S52525	probable membrane
18	343.5	5.5	845	2	T25657	hypothetical prote
19	340	5.4	881	2	T31739	hypothetical prote
20	317.5	5.1	800	2	T26683	hypothetical prote
21	314	5.0	877	2	T24097	hypothetical prote
22	309	4.9	820	2	T32908	hypothetical prote
23	300	4.8	983	2	T21213	hypothetical prote
24	293.5	4.7	1456	2	T15961	hypothetical prote
25	291	4.6	840	2	T33217	hypothetical prote
26	275.5	4.4	871	2	T28706	hypothetical prote
27	261.5	4.2	890	2	T22186	hypothetical prote
28	258.5	4.1	690	2	T23399	hypothetical prote
29	188	3.0	1276	2	T18526	SREBP cleavage act
30	183	2.9	1028	2	H71918	probable efflux tr
31	176.5	2.8	746	2	A75018	transport protein
32	175	2.8	1028	2	G64595	acriflavine resist
33	174.5	2.8	633	2	S44795	F09G8.3 protein -
34	173	2.8	787	2	H71453	hypothetical prote
35	168.5	2.7	888	2	E71280	probable antibioti
36	168	2.7	932	2	T28820	hypothetical prote
37	166	2.6	1077	2	H96007	probable acriflavi
38	164.5	2.6	1154	2	T48829	related to SREBP c
39	163.5	2.6	1028	2	AD0052	probable multi-dru
40	161	2.6	1027	2	F82829	acriflavin resista
41	157	2.5	1053	2	D83206	probable RND efflu
42	153.5	2.4	847	2	T34577	probable export pr
43	151	2.4	736	1	C69307	conserved hypothet
44	149	2.4	749	2	H91170	hypothetical membr
45	148	2.4	772	2	H86016	hypothetical prote

ALIGNMENTS

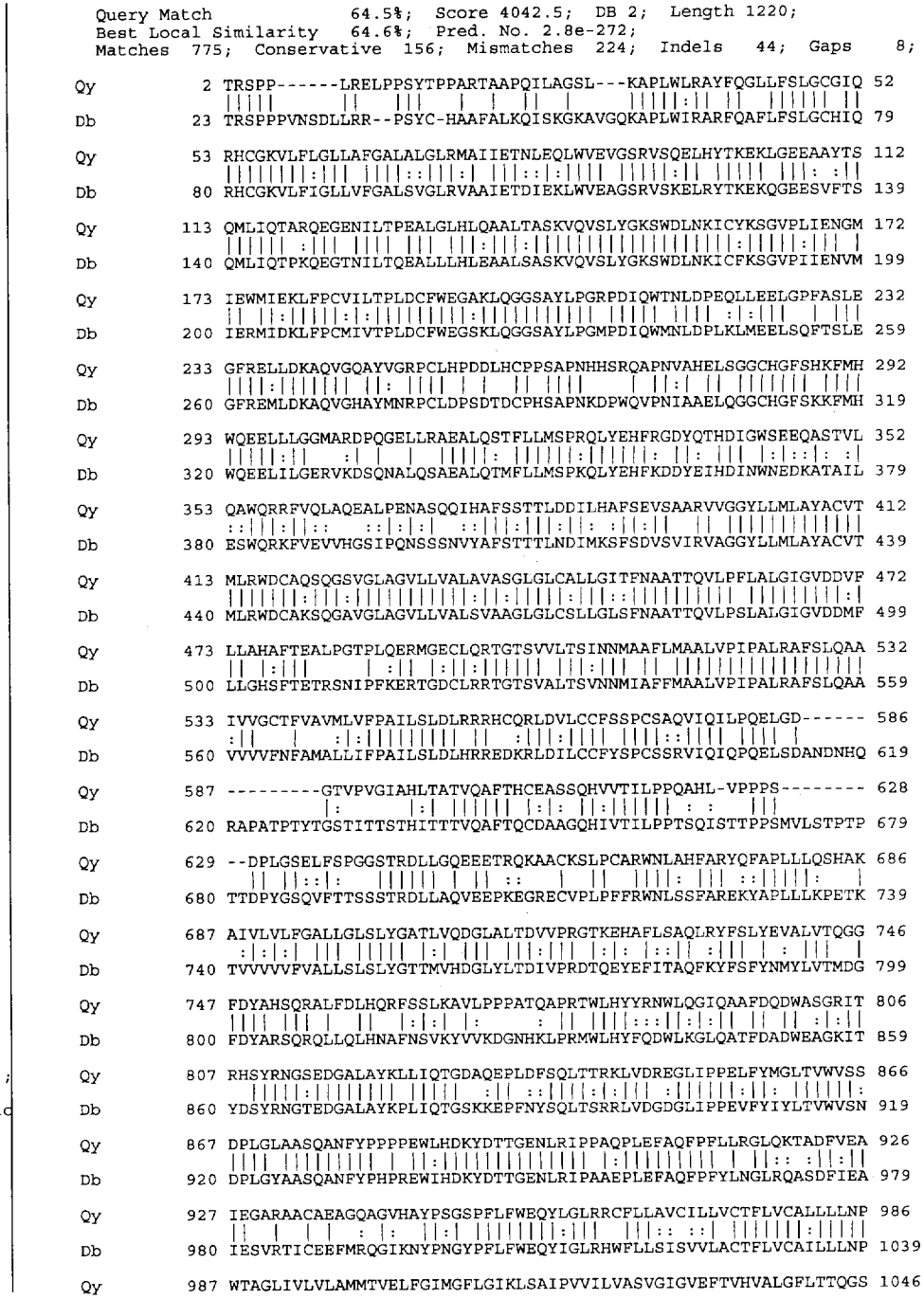
RESULT 1
T13952
membrane protein ptch2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13952
R;Motoyama, J.; Takabatake, T.; Takeshima, K.; Hui, C.
Nature Genet. 18, 104-106, 1998
A;Title: Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog.
A;Reference number: Z17830; MUID:98122566; PMID:9462734
A;Accession: T13952
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1182 <MOT>
A;Cross-references: UNIPROT:O35595; EMBL:AB010833; PIDN:BAA24691.1
A;Experimental source: strain BALB/cCrSlc
C;Genetics:
A;Gene: ptch2
C;Superfamily: Drosophila membrane protein patched
C;Keywords: transmembrane protein

Query Match 89.3%; Score 5599; DB 2; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              | |   | ||||||||||||::|| |||||:||||||||||||||||| ||:||||||
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              |||:||||||||||:|:|||:|||||||||||||||||||||||||||||||||||||||
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||| |:|||||| ||||||||||||||||||||||||||||||||||||||||| |||||
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              |||||||||||||| ||| |||||||| ||||||||| ||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              | ||| ||:|||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              |||||||| |||||||||||||||||| |||||| ||||||||||||||||||||||||||
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420
```



RESULT 2
T18291
patched protein - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18291
R;Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;
Development 122, 2835-2846, 1996
A;Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic
A;Reference number: Z18860; MUID:96379744; PMID:8787757
A;Accession: T18291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1220 <CON>
A;Cross-references: UNIPROT:Q98864; EMBL:X98883; PIDN:CAA67386.1
C;Genetics:
A;Gene: ptc1
C;Superfamily: Drosophila membrane protein patched



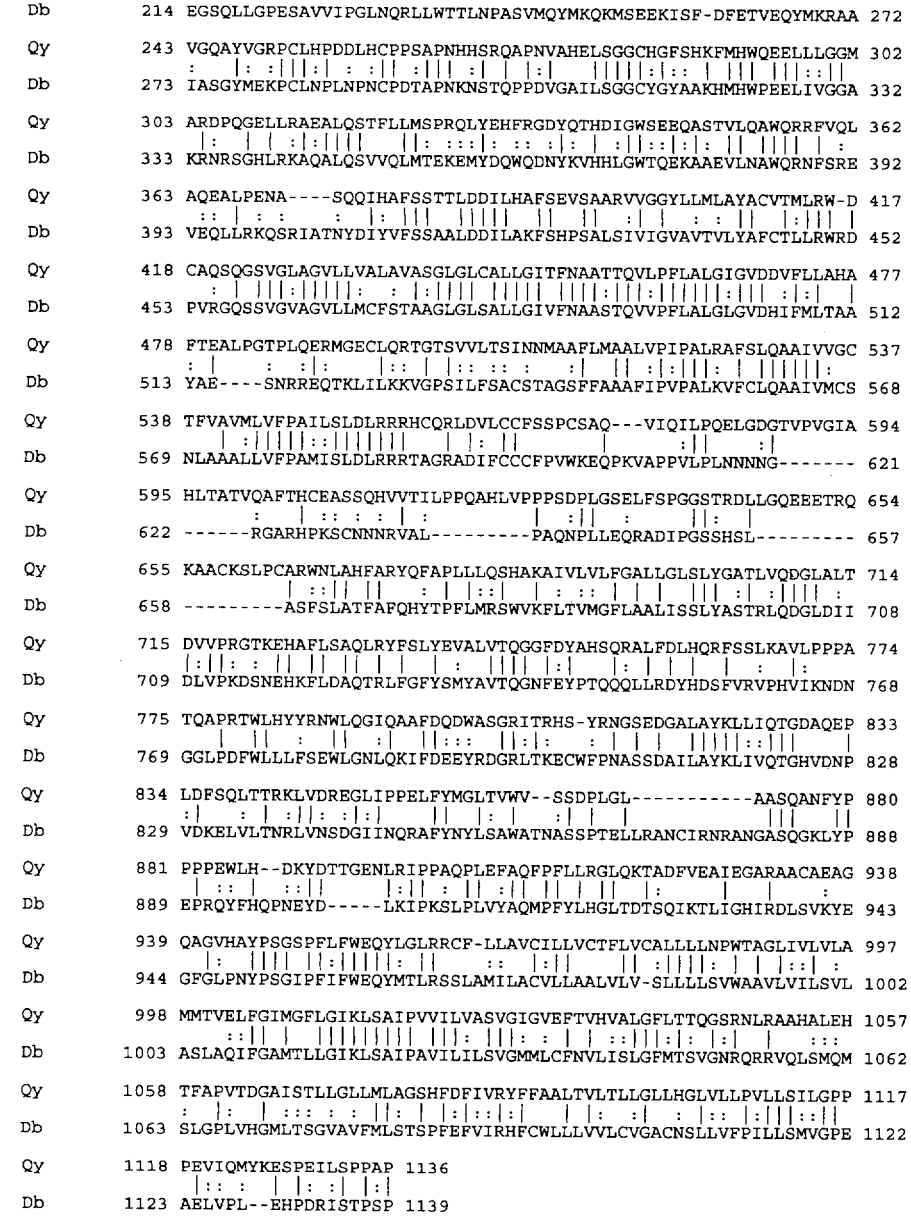
```
Db       1040 WTAGVIVFILPMMTVELFGIMGLIGIKLSAIPVVILIASVGIGVEFTVHIALGFLTAIGD 1099

Qy       1047 RNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVL 1106

Db       1100 RNTRSAVAMEHMFAPVIDGAISTLLGVLMLAGSEFDFIMRYFFAVLAILTLLGILNGLVL 1159

Qy       1107 LPVLLSILGPPPEVI------QMYKESPEILSPPAPQGGGLRWGASSSLPQSFARVTTS 1159

Db       1160 LPVLLSLMGPPAEVVPANNANHLQSPSPEPMPPPMNHHGYYAGHIPKASHQAFSETSDS 1218


RESULT 3
T18538
patched protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18538
R;Marigo, V.; Scott, M.P.; Johnson, R.L.; Goodrich, L.V.; Tabin, C.
Development 122, 1225-1233, 1996
A;Title: Conservation in hedgehog signaling: induction of a chicken patched homolog by S
A;Reference number: Z18958; MUID:96205046; PMID:8620849
A;Accession: T18538
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1442 <MAR>
A;Cross-references: UNIPROT:Q90693; EMBL:U40074; NID:g1335850; PID:g1335851; PIDN:AAC598
C;Genetics:
A;Gene: PTC
C;Superfamily: Drosophila membrane protein patched
C;Keywords: transmembrane protein

  Query Match             53.3%;  Score 3340;  DB 2;  Length 1442;
  Best Local Similarity   54.3%;  Pred. No. 2.1e-223;
  Matches  663;  Conservative  204;  Mismatches  304;  Indels   50;  Gaps   17;

Qy         12 PSYTPPARTAAPQILAG---SLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68

Db         54 PSYC-DAAFALEQIAKGRATGRRAPLWLRAKFQRLLFNLGCYIQKNCGKFLVVGLL-YSA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128

Db        112 FAVGLRAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPQEDGTNVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188

Db        172 TEALRQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITEAGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247

Db        232 LDCFWEGAKLQSGTAYLLGKPPLQWINFDPLEFLEELKKINYQVESWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307

Db        292 MDRPCLNPADPDCPITAPNKNSTKPLDVALVLSGGCYGLSRKYMHWQEELIIGGTVKNSS 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366

Db        352 GKLVSAQALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRMYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426

Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCAKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484

Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544

Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------GTVPVGIAH--- 595

Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVTRVIQIEPQAYAENDNICYSSPPPYSSHSFA 650

Qy        596 ------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRDL 645

Db        651 HETQITMQSTVQLRTEYDPHTQAYYTTAEPRSEISVQPVTVTQDSLSCQSPESASSTRDL 710

Qy        646 LGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGAT 705

Db        711 LSQFSDS--SVHCLEPPCTKWTLSTFAEKHYAPFLLKPKAKVVVIFLFLGLLGLSLYGTT 768

Qy        706 LVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSS 765

Db        769 RVRDGLDLTDIVPRDTREYDFIAAQFKYFSFYNMYIVTQKA-DYPNVQHLLYELHRSFSN 827

Qy        766 LKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLI 825

Db        828 VTYVLLEGDRQLPKMWLHYFRDWLQGLQDAFDSDWETGKITYSNYKNGSDDAVLAYKLLV 887

Qy        826 QTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEW 885

Db        888 QTGNRAKPIDISQLTKQRLVDADGIINPNAFYIYLTAWVSNDPVAYAASQANIRPHRPEW 947

Qy        886 LHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHA 944

Db        948 VHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRETSDFVEAIEKVRAICNNYTSLGIAS 1007

Qy        945 YPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELF 1004

Db       1008 YPNGYPFLFWEQYIGLRHWLLLSISVVLACTFLVCALFLLNPWTAGIIVVVLALMTVELF 1067

Qy       1005 GIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTD 1064

Db       1068 GMMGLIGIKLSAVPVVILIASVGIGVEFTVHIALAFLTAIGDKNRRAVLALEHMFAPVLD 1127

Qy       1065 GAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI--- 1121

Db       1128 GAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPAC 1187

Qy       1122 ---QMYKESPEILSPPA------PQGGGLRWGASSSLPQSFARVTTSMTVAIH---PPPL 1169

Db       1188 GRNRLPTPSPE--PPPSIVRFALPPGHTNNGSDSSDSEYSSQTTVSGISEELHHYEATQS 1245

Qy       1170 PGAYIHPAPDEPPWSPAATSS 1190

Db       1246 PGIPVHQVVVEATENPVFARS 1266


RESULT 4
T30172
transmembrane protein patched - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30172
R;Goodrich, L.V.; Johnson, R.L.; Milenkovic, L.; McMahon, J.A.; Scott, M.P.
Genes Dev. 10, 301-312, 1996
A;Title: Conservation of the hedgehog/patched signaling pathway from flies to mice: indu
A;Reference number: Z20752; MUID:96176226; PMID:8595881
A;Accession: T30172
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1434 <GOO>
A;Cross-references: UNIPROT:Q61115; EMBL:U46155; NID:g1181884; PID:g1181885; PIDN:AAC987
A;Experimental source: clone M2, M9
C;Superfamily: Drosophila membrane protein patched

  Query Match             53.2%;  Score 3337;  DB 2;  Length 1434;
  Best Local Similarity   53.1%;  Pred. No. 3.4e-223;
  Matches  672;  Conservative  206;  Mismatches  309;  Indels   78;  Gaps   20;

Qy          3 RSPPLREL--PPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGK 57

Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86
```

```
Qy        58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
Db        87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy       118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177
Db       147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy       178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236
Db       207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy       237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296
Db       267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy       297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355
Db       327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy       356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415
Db       386 QRTYVEVVHQSVAPNSTQKVLPFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445

Qy       416 WDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLA 475
Db       446 WDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLA 505

Qy       476 HAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533
Db       506 HAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAV 565

Qy       534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------- 586
Db       566 VVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTEPHSNTRY 625

Qy       587 GTVPVGIAH---------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS 633
Db       626 SPPPPYTSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDNLSC 685

Qy       634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLF 693
Db       686 QSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVILLF 743

Qy       694 GALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQ 753
Db       744 LGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQ 802

Qy       754 RALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNG 813
Db       803 HLLYDLHKSFSNVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNNYKNG 862

Qy       814 SEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAA 873
Db       863 SDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAA 922

Qy       874 SQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA 932
Db       923 SQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRV 982

Qy       933 ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLI 992
Db       983 ICNNYTSLGLSSYPNGYPFLFWEQYISLRHWLLLSISVVLACTFLVCAVFLLNPWTAGII 1042

Qy       993 VLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAA 1052
Db      1043 VMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNHRAM 1102

Qy      1053 HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLS 1112
Db      1103 LALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPVLLS 1162

Qy      1113 ILGPPPEVI------QMYKESPEILSPP-----APQGGGLRWGASSSLPQSFARVTTS-- 1159
Db      1163 FFGPCPEVSPANGLNRLPTPSPE--PPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220

Qy      1160 --------------------MTVAIHPPPLPGAYIHP-APDEPPWSPAA---TSSGNLS 1194
Db      1221 SEELRQYEAQQGAGGPAHQVIVEATENPVFARSTVVHPDSRHQPPLTPRQQPHLDSGSLS 1280

Qy      1195 SRGPG 1199
Db      1281 ---PG 1282
```

RESULT 5
S06119
membrane protein patched - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: S06119; A33468
R;Nakano, Y.; Guerrero, I.; Hidalgo, A.; Taylor, A.; Whittle, J.R.S.; Ingham, P.W.
Nature 341, 508-513, 1989
A;Title: A protein with several possible membrane-spanning domains encoded by the Drosop
A;Reference number: S06119; MUID:90015164; PMID:2797178
A;Accession: S06119
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1299 <NAK>
A;Cross-references: UNIPROT:P18502; GB:X17558; NID:g8389; PIDN:CAA35591.1; PID:g8390
R;Hooper, J.E.; Scott, M.P.
Cell 59, 751-765, 1989
A;Title: The Drosophila patched gene encodes a putative membrane protein required for se
A;Reference number: A33468; MUID:90058658; PMID:2582494
A;Accession: A33468
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-110,'R',112-273,'G',275-331,'R',333-635,'P',637-861,'DVF',878,'Y',880-1299
A;Cross-references: GB:M28418; GB:M28999; NID:g552097; PID:g552099
C;Genetics:
A;Gene: FlyBase:ptc
A;Cross-references: FlyBase:FBgn0003892
A;Map position: 2 44D3-D4
C;Superfamily: Drosophila membrane protein patched
C;Keywords: glycoprotein; transmembrane protein
F;74-92/Domain: transmembrane #status predicted <TM01>
F;427-448/Domain: transmembrane #status predicted <TM02>
F;456-503/Domain: transmembrane #status predicted <TM03>
F;529-555/Domain: transmembrane #status predicted <TM04>
F;557-585/Domain: transmembrane #status predicted <TM05>
F;677-699/Domain: transmembrane #status predicted <TM06>
F;967-1017/Domain: transmembrane #status predicted <TM07>
F;1019-1047/Domain: transmembrane #status predicted <TM08>
F;1061-1086/Domain: transmembrane #status predicted <TM09>
F;1093-1121/Domain: transmembrane #status predicted <TM10>
F;142,298,335,388,807,861,1194,1271/Binding site: carbohydrate (Asn) (covalent) #status

  Query Match   31.3%; Score 1961.5; DB 1; Length 1299;
  Best Local Similarity 37.0%; Pred. No. 9.3e-128;
  Matches 429; Conservative 225; Mismatches 412; Indels   93; Gaps   21;

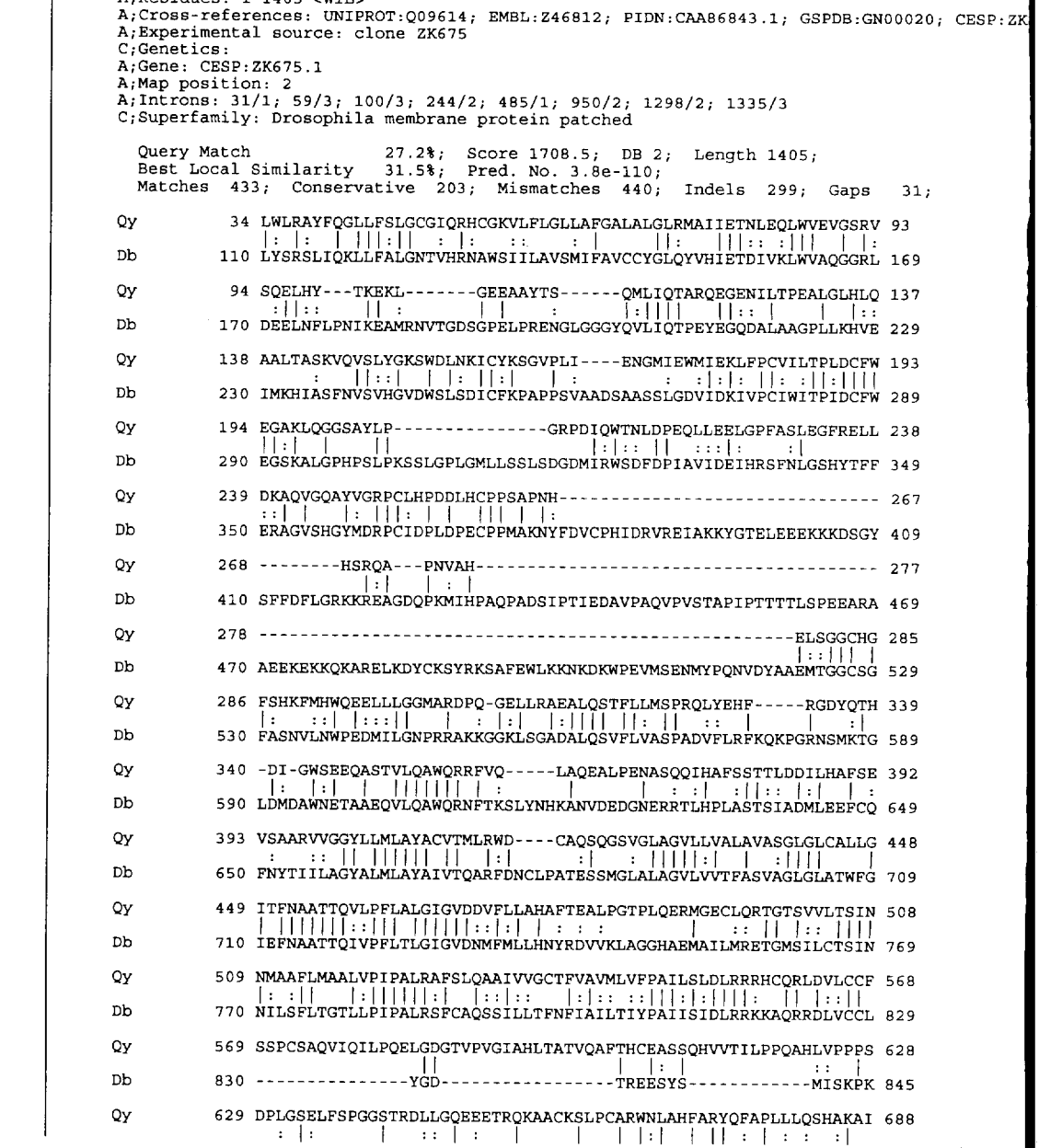
```
Qy        18 ARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGALALGLR 74
Db        34 AQVALDQIDKGKARGSRTAIYLRSVFQSHLETLGSSVQKHAGKVLFVAILVLSTFCVGLK 93

Qy        75 MAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILTPEALGL 134
Db        94 SAQIHSKVHQLWIQEGGGLEAELAYTQKTIGEDESATHQLLIQTTHDPNASVLHPQALLA 153

Qy       135 HLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIEN-GMIEWMIEKLFPCVILTPLDCFW 193
Db       154 HLEVLVKATAVKVHLYDTEWGLRDMCNMPSTPSFEGIYYIEQILRHLIPCSIITPLDCFW 213

Qy       194 EGAKLQG--GSAYLPG-RPDIQWTNLDP--------EQLLEELGPFASLEGFRELLDKAQ 242
```



RESULT 6
T27969
hypothetical protein ZK675.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27969

R;Sims, M.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z20448
A;Accession: T27969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1405 <WIL>
A;Cross-references: UNIPROT:Q09614; EMBL:Z46812; PIDN:CAA86843.1; GSPDB:GN00020; CESP:ZK
A;Experimental source: clone ZK675
C;Genetics:
A;Gene: CESP:ZK675.1
A;Map position: 2
A;Introns: 31/1; 59/3; 100/3; 244/2; 485/1; 950/2; 1298/2; 1335/3
C;Superfamily: Drosophila membrane protein patched

Query Match 27.2%; Score 1708.5; DB 2; Length 1405;
Best Local Similarity 31.5%; Pred. No. 3.8e-110;
Matches 433; Conservative 203; Mismatches 440; Indels 299; Gaps 31;



```
Db        846 --IQSKRIIGAPSEASIMQQFDGITQAQMASSDDPAPWSLHSFIRYYYIPFISKPASKVA 903

Qy        689 VLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQG-GF 747

Db        904 IIVGCCALLGASFIGMRQSTLGLELGDVLPEHTAPAQFLRARDKYFSFYPMFAVIKGPNI 963

Qy        748 DYAHSQRALFDLHQRFSSLKAVLPPPATQ-APRTWLHYYRNWLQGIQAAFDQDWASGRIT 806

Db        964 DYAHQQRQIDNYRQSIGSSKYVIKNKNEEPSEKYWLGLMRDWLISIQRGFDEEVAKGSFN 1023

Qy        807 RHS----YRNGSEDGALAYKLLIQTGDAQEPLDF---SQLTTRKLVDREGLIPPELFYMG 859

Db       1024 LTSGTVIGSNVSEDARLAHALMCSHGSL-----FGCAGRVGKIRLVDASGIINSDGFYNY 1078

Qy        860 LTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLLRGLQK 919

Db       1079 LTAWFNVDHMMYYVSQASFFPTPPKWELSKNHT--ENF-IPAAEPLAYSQIPFYLTGLTD 1135

Qy        920 TADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVC 979

Db       1136 TAVIVDAIKDIRSVCERFTDQGLPNFPQGIAFTFWEQYLFLTGNLMQAISIITISVFCVI 1195

Qy        980 ALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALG 1039

Db       1196 SVLLFNPWAALMVVCILGIMTCELAGFMGLVGIKLNPVSAVTLITAVGIGVEFTVHVVVS 1255

Qy       1040 FLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLG 1099

Db       1256 FLTALGTRSQRTSSAVDRVFVPVIHGSFSTLLGILMLGFSEFEFVVKYFFIVMTALICIG 1315

Qy       1100 LLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLPQSFARVTTS 1159

Db       1316 IINGLILLPVLLSWFGPRREI--------------SPTGG-----------------KTT 1344

Qy       1160 MTVAIHPPPLP--------GAYIHPAPDEPP----WSPAA-----TSSGNLSSRG 1197

Db       1345 LTL---PPPLPKNANSSRSGGDDSDEDDEPSGLVMYSRQAPPTTRTSGGNRGTVG 1396
```

RESULT 7
T16126
hypothetical protein F21H12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16126
R;Favello, T.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F21H12.
A;Reference number: Z18464
A;Accession: T16126
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-714 <FAV>
A;Cross-references: UNIPROT:Q09540; EMBL:U23176; NID:g726404; PID:g726409; PIDN:AAC46717
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F21H12.4
A;Introns: 25/1; 334/2; 430/2; 543/3

  Query Match 15.8%; Score 992; DB 2; Length 714;
  Best Local Similarity 31.4%; Pred. No. 8.5e-61;
  Matches 256; Conservative 116; Mismatches 280; Indels 164; Gaps 13;

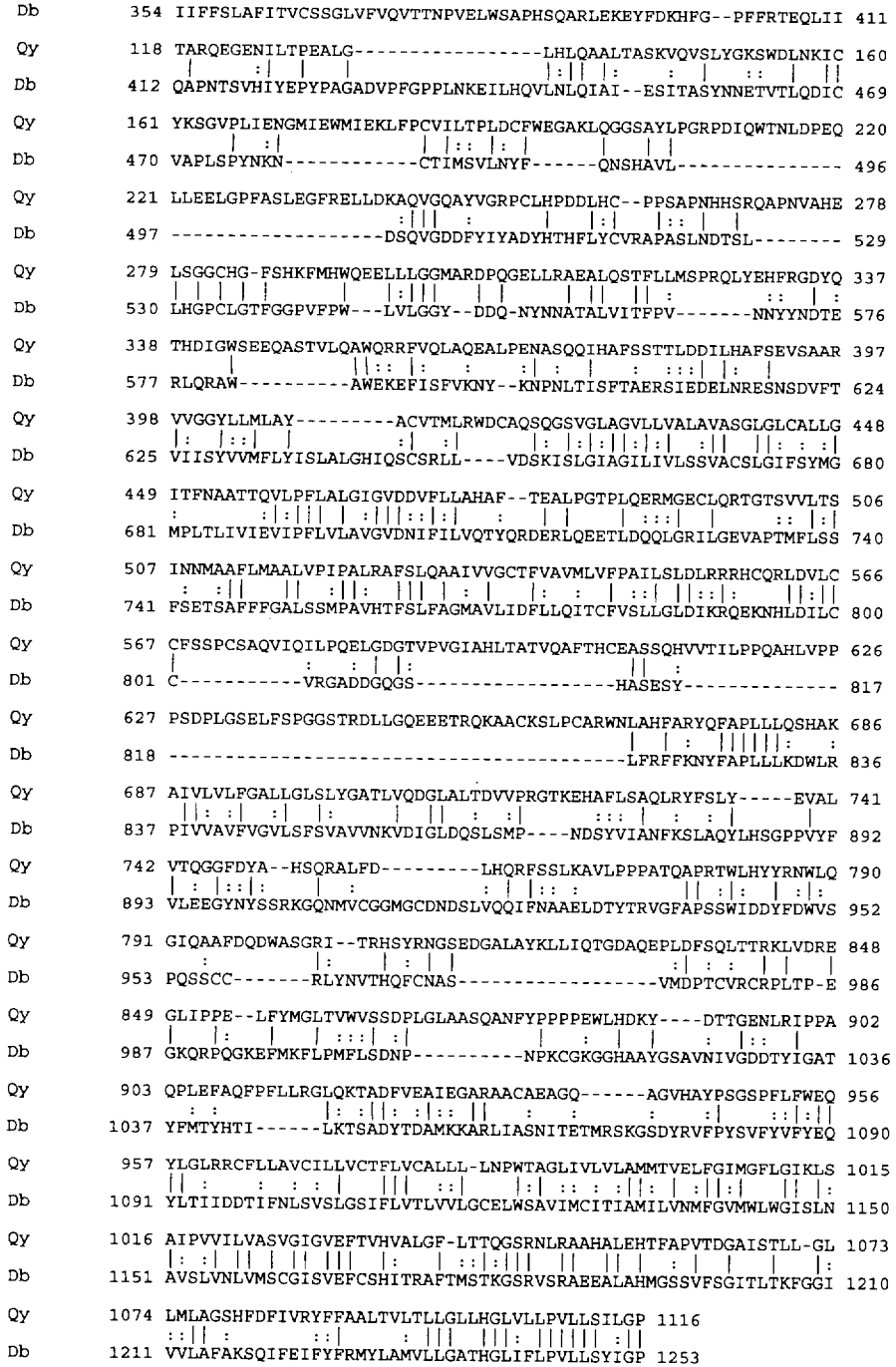
```
Qy        271 QAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ-GELLRAEALQSTFLLMSPRQLY 329

Db         55 QNVDYAAEMTGGCSGFASNVLNWPEDMILGNPRRAKKGGKLSGADALQFVFLVASPADVF 114

Qy        330 EHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHA 389

Db        115 LRFK---------QSLEETLETLSLYEEHCIHLHRHPLLICSRNSVNSTIPSSLLDMLSC 165

Qy        390 FSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGI 449
```

```
Db        166 WH----------MLLLLILDLTTAFR--LQNHQWGFALAGVLVVTFASVAGIGLATWFGI 213

Qy        450 TFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSINN 509

Db        214 EFNAATTQIVPFLTLGIGVDNMFMLLHNYRDVVKLAGGHAEMAILMRETGMSILCTSINN 273

Qy        510 MAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFS 569

Db        274 ILSFLTGTLLPIPALRSFCAQSSILLTFNFIAILTIYPAIISIDLRRKKAQRRDFDTREE 333

Qy        570 SPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLVPPPSD 629

Db        334 STSEASIMQQF-----DG---------------ITQAQMASS----------------DD 357

Qy        630 PLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIV 689

Db        358 P--------------------------------APWSLHSFIRYYYIPFISKPASKVAI 384

Qy        690 LVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQG-GFD 748

Db        385 IVGCCALLGASFVGMRQSTLGLELGDVLPEHTAPAQFLRARDKYFSFYPMFAVIKGPNID 444

Qy        749 YAHSQRALFDLHQRFSSLKAVLPPPATQ-APRTWLHYYRNWLQGIQAAFDQDWASGRITR 807

Db        445 YAHQQRQIDNYRQSIGSSKYVIKNKNEEPSEKYWLGLMRDWLISIQRGFDEEVAKGSFNL 504

Qy        808 HS----YRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVW 863

Db        505 TSGTVIGSNVSEDARLAHALMCSHGSLFE-----------CAGRIGKI------------ 541

Qy        864 VSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLLRGLQKTADF 923

Db        542 ---------------------------------------------RLIPFYLTGLTDTAVI 557

Qy        924 VEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLL 983

Db        558 VDAIKDIRSVCERFTDQGLPNFPQGIAFTFWEQYLFLTGNLMQAISIITISVFCVISVLL 617

Qy        984 LNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTT 1043

Db        618 FNPWAALMVVCILGIMTCELAGFMGLVGIKLNPVSAVTLITAVGIGVEFTVHVVVSFLTA 677

Qy       1044 QGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGS 1079

Db        678 LGTRSQRTSSAVDRVFVPVIHGSFSTLLGILMLGFS 713
```

RESULT 8
T30188
Niemann-Pick C disease protein - mouse
N;Alternate names: NCP1 protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30188
R;Loftus, S.K.; Morris, J.A.; Carstea, E.D.; Gu, J.Z.; Cummings, C.; Brown, A.; Ellison,
Science 277, 232-235, 1997
A;Title: Murine model of niemann-pick C disease: mutation in a cholesterol homeostasis g
A;Reference number: Z20765; MUID:97362324; PMID:9211850
A;Accession: T30188
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1278 <LOF>
A;Cross-references: UNIPROT:O35604; EMBL:AF003348; NID:g2251241; PID:g2251242; PIDN:AAB6
C;Genetics:
A;Gene: Npc1
A;Map position: 18

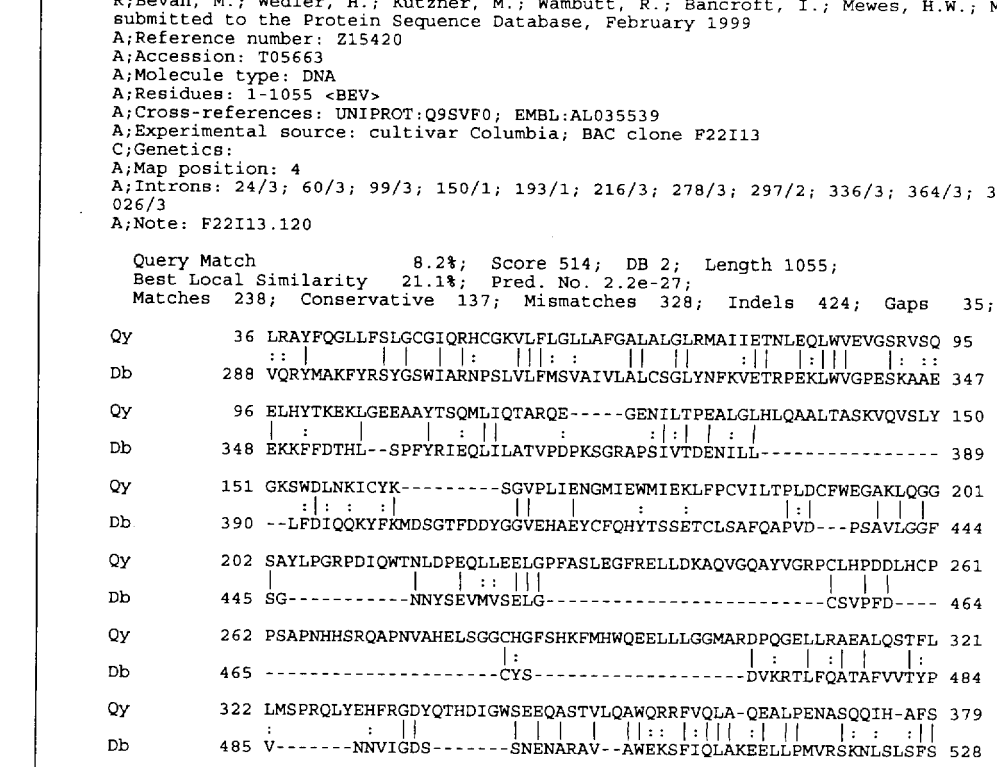
  Query Match 9.6%; Score 602.5; DB 2; Length 1278;
  Best Local Similarity 22.4%; Pred. No. 2.1e-33;
  Matches 252; Conservative 174; Mismatches 410; Indels 287; Gaps 37;

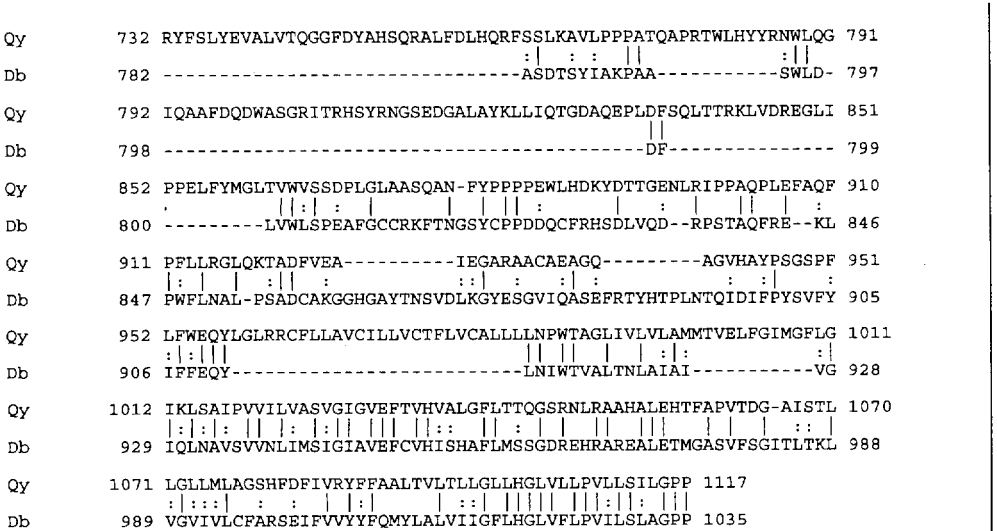
```
Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
```



RESULT 9
T05663
hypothetical protein F22I13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05663
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Accession: T05663
A;Molecule type: DNA
A;Residues: 1-1055 <BEV>
A;Cross-references: UNIPROT:Q9SVF0; EMBL:AL035539
A;Experimental source: cultivar Columbia; BAC clone F22I13
C;Genetics:
A;Map position: 4
A;Introns: 24/3; 60/3; 99/3; 150/1; 193/1; 216/3; 278/3; 297/2; 336/3; 364/3; 396/3; 419/3; 026/3
A;Note: F22I13.120

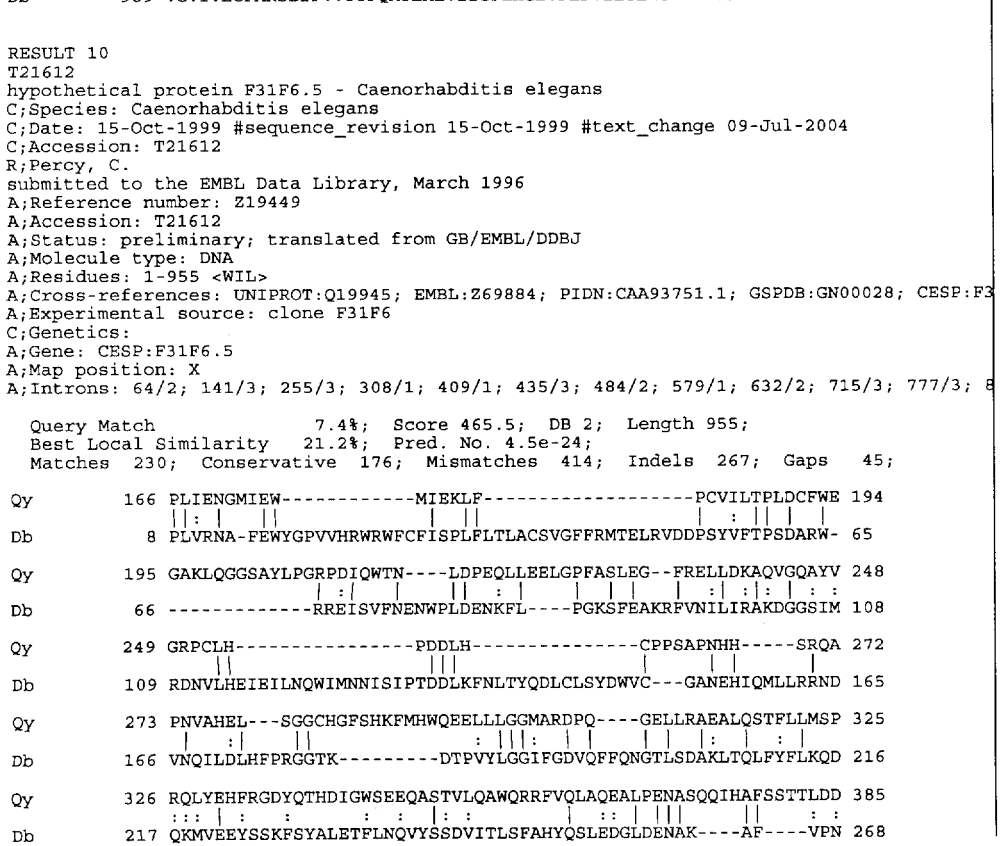
Query Match 8.2%; Score 514; DB 2; Length 1055;
Best Local Similarity 21.1%; Pred. No. 2.2e-27;
Matches 238; Conservative 137; Mismatches 328; Indels 424; Gaps 35;

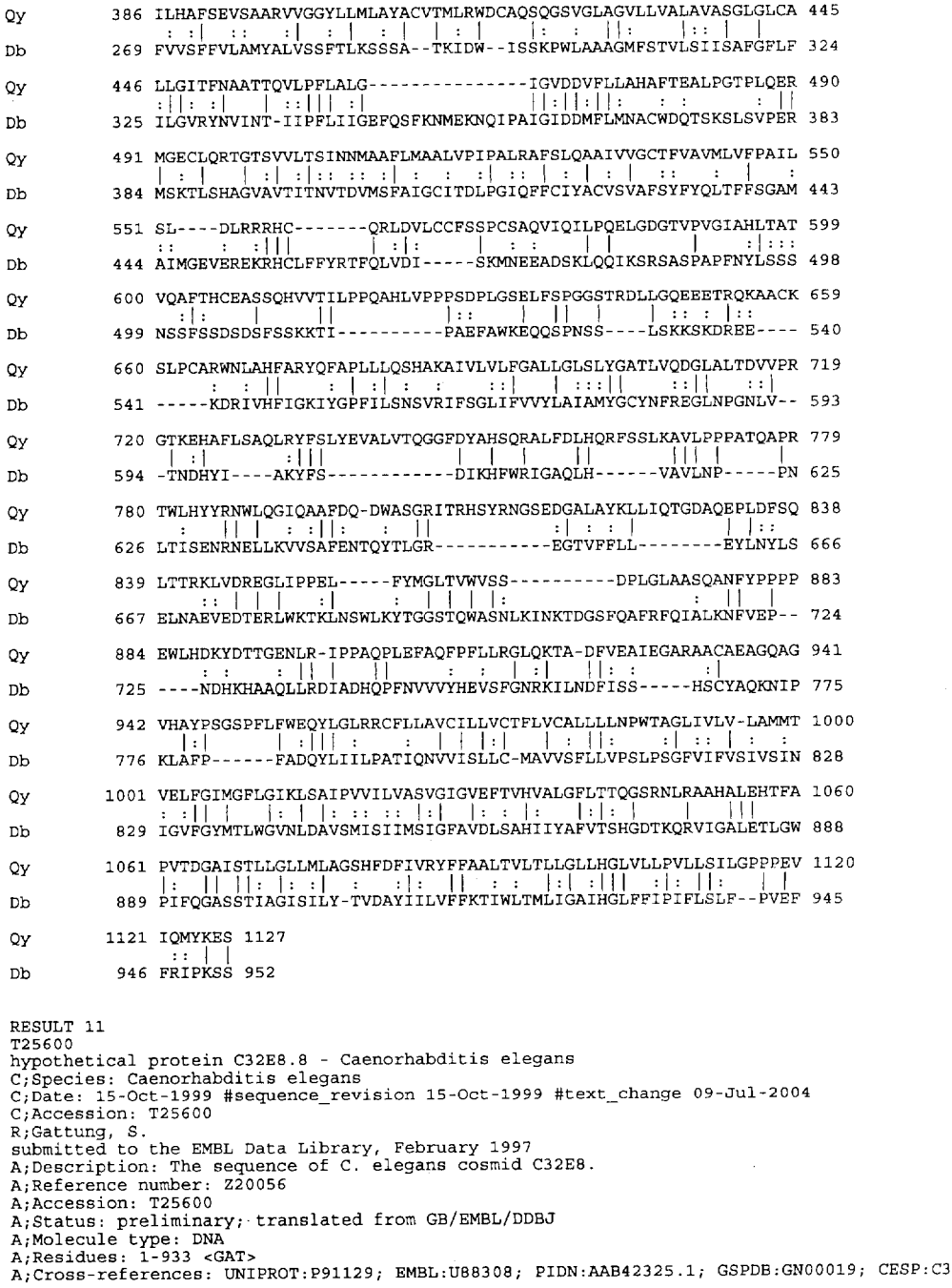




RESULT 10
T21612
hypothetical protein F31F6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21612
R;Percy, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19449
A;Accession: T21612
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-955 <WIL>
A;Cross-references: UNIPROT:Q19945; EMBL:Z69884; PIDN:CAA93751.1; GSPDB:GN00028; CESP:F3
A;Experimental source: clone F31F6
C;Genetics:
A;Gene: CESP:F31F6.5
A;Map position: X
A;Introns: 64/2; 141/3; 255/3; 308/1; 409/1; 435/3; 484/2; 579/1; 632/2; 715/3; 777/3; 8

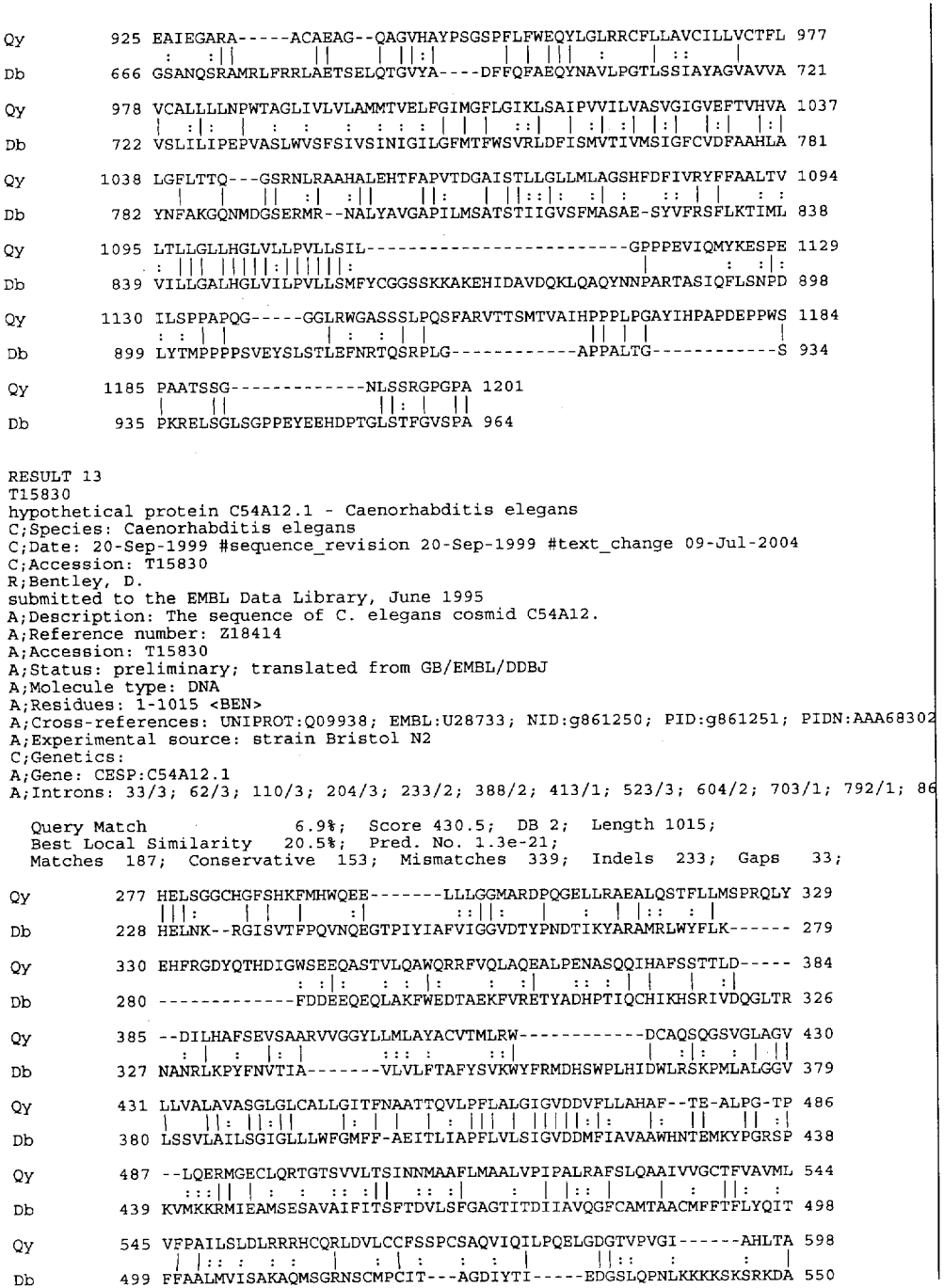
Query Match 7.4%; Score 465.5; DB 2; Length 955;
Best Local Similarity 21.2%; Pred. No. 4.5e-24;
Matches 230; Conservative 176; Mismatches 414; Indels 267; Gaps 45;





RESULT 11
T25600
hypothetical protein C32E8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25600
R;Gattung, S.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C32E8.
A;Reference number: Z20056
A;Accession: T25600
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-933 <GAT>
A;Cross-references: UNIPROT:P91129; EMBL:U88308; PIDN:AAB42325.1; GSPDB:GN00019; CESP:C3

```
A;Experimental source: strain Bristol N2; clone C32E8
C;Genetics:
A;Gene: CESP:C32E8.8
A;Map position: 1
A;Introns: 145/1; 177/2; 385/1; 418/3; 833/3; 878/3

  Query Match             7.1%;  Score 444;  DB 2;  Length 933;
  Best Local Similarity   21.4%;  Pred. No. 1.4e-22;
  Matches  217;  Conservative  170;  Mismatches  398;  Indels  228;  Gaps   37;

Qy        204 YLPGRP-----DIQWTNL--DPEQLLEELGPFASLEGFRELLDKAQV---GQAYVGRP-C 252
Db         81 YIPGRAVTQSREIQVTALARNDSNILDPKFANAVYQLDKYIQTRVRVLHNGHYYSYKNLC 140

Qy        253 LHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGF--SHKFMHWQEELLLGGMARDPQGEL 310
Db        141 LQYKNGGCPSNKHVHILSDLHN---------HGFNITYPYFRFGSE---GGYIGSSLGGV 188

Qy        311 LRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPEN 370
Db        189 TVMKGENETDILASAKAW-------FMIYHLKFHPEEMSYISGEWELELGRMLTQ-YPED 240

Qy        371 ASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRW-------DCAQSQG 423
Db        241 PYISITYFHSQTLADELKRNADTLIPRFIISITLLIVFSTLCSLSFIDGSFSIDWVLSKP 300

Qy        424 SVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALP 483
Db        301 ILSILGVVSAGIAILTGVGFLSLMGMPYN-DIVGVMPFLVLAVGVDNMFLMVAAVRRTSR 359

Qy        484 GTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVM 543
Db        360 THTVHERMGECLADAAVSILITSSTDVLSFGVGAITTIPAVQIFCVYTGVAIFFAFIYQI 419

Qy        544 LVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-GTVPVGIAHLTATVQA 602
Db        420 TFFAACLALAMKHEASGRNSLFLIEAVSAEKKTSLSTFQRLFNLGSVP------------ 467

Qy        603 FTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLP 662
Db        468 ----DHSASHDV-------------KQPLTSRFF------------------------- 484

Qy        663 CARWNLAHFARYQFAPLLLQSHAKAIVLVLFGA-LLGLSLYGATLVQDGLALTDVVPRGT 721
Db        485 -GEW---------YAPVLMHPVVRGIAMVWFVIYLLGAS-YGCSRIKEGLEPVNLLVEDS 533

Qy        722 KEHAFLSAQLRYFSLY--EVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPR 779
Db        534 YAIPHYRLLEKYFWKYGQQVQIVINNAPDLRN--------HTSRDRVHAMVLDFATSKHA 585

Qy        780 TWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQL 839
Db        586 IGMESVQFWLFEMERYYQKELEVQIIDSSFY------GLLHHFLASKT------------ 627

Qy        840 TTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRI 899
Db        628 -------------------------NNPL----AEDIYWGPMPD------DDNGTMVK- 650

Qy        900 PPAQPLEFAQFPFLL--RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP-FLFWEQ 956
Db        651 ---------SFRFILGMKDLVTTMDQTDATMSFREVAARWPEFNVTTF---MPIWMFTDQ 698

Qy        957 YLGLRRCFLLAVCILLVCTFLVCALLLLNP----WTAGLIVLVLAMMTVELFGIMGFL-- 1010
Db        699 YIIIIPNTVQNIIIALLVMIVIAVLFIPQPMCSLWVA------LACASID-FGVIGYMTL 751

Qy       1011 -GIKLSAIPVVILVASVGIGVEFTVHVALGFLTT-QGSRNLRAAHALEHTFAPVTDGAIS 1068
Db        752 WGVNLDAISMITIIMSIGFSVDYSAHIAYGYVVSREDTAAGRVKEALSALGWPLSQGAMS 811

Qy       1069 TLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSIL-----------GP 1116
Db        812 TIIAVSVLADIPAYMIVT-FFKTVVLSISLGLLHGLVFLPVLLSIFVRGCCIIPSSPHGH 870

Qy       1117 PPEV-------IQMYKESPEILSPPAPQGGGLRWGASSSLPQSFARVTTSMTV 1162
Db        871 PSAQKIEKQIRIAAISSSPLDLRTVAP----LRASSPISFPHRLEYTDESPTV 919


RESULT 12
T26746
hypothetical protein Y39A1B.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26746
R;Wall, M.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20258
A;Accession: T26746
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1003 <WIL>
A;Cross-references: UNIPROT:Q9XXR9; EMBL:AL021482; PIDN:CAA16339.1; GSPDB:GN00021; CESP:
A;Experimental source: clone Y39A1B
C;Genetics:
A;Gene: CESP:Y39A1B.2
A;Map position: 3
A;Introns: 89/2; 126/3; 167/2; 194/2; 232/1; 266/3; 295/2; 323/2; 363/1; 519/3; 696/3; 7

  Query Match             7.1%;  Score 444;  DB 2;  Length 1003;
  Best Local Similarity   21.6%;  Pred. No. 1.5e-22;
  Matches  214;  Conservative  131;  Mismatches  333;  Indels  312;  Gaps   34;

Qy        285 GFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWS 344
Db        214 GMTH---------LLGGVTLDDDKRIAGAKAMLLPYALR-----------HSSDDEDW- 251

Qy        345 EEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLL 404
Db        252 ------VAEKWE---VRLA-DFLLQYDSPIIRA-SWWTYETLA---AESARDRLQLIHML 297

Qy        405 MLAYACVTMLRWDCA------QSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQV 458
Db        298 LPCFVCVSIFTIACCCVFSWRRSRPWLAIGGVISAAMAIASAVGILLLAGYGMTSVAYS- 356

Qy        459 LPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAAL 518
Db        357 MPFIVFSVGVDNVFILLSAWRSTSSTETLEHRMKETFADAAVSITVTSLTDLISFGVGCA 416

Qy        519 VPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRR----RHCQRLDVLCCFSSPCSA 574
Db        417 TPFPSVQMFCAYAVAAVIFTYIYQLTFFAAVMVYTNRREINNRHC--------------- 461

Qy        575 QVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSE 634
Db        462 ----IFFHKLKKDTLPEKIA---------------------------------------- 477

Qy        635 LFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFG 694
Db        478 ------------AQGDRSFEKNTI---------LAQFFRTTYSDFLLNPLVRIVILVTFC 516

Qy        695 ALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQR 754
Db        517 VYLGVASYGCTKVKLGLEPNDLLPENSYGKRTLMMAEKYFS------------DYGSS-- 562

Qy        755 ALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW----ASGRITRHSY 810
Db        563 --------------------------LHVWMYNLSEVDVAPRKIWNVLEKEVELYEHTE 595

Qy        811 RNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREG-LIPPELF-YMGLTVWVSSDP 868
Db        596 FTASSDSWLR-------------------TFLAFVKQAGLLITPENFVYILKNVFLSQ-- 634

Qy        869 LGLAASQANFYPPPPEWLHDKYDTT----GENLRIPPAQPLEFAQFPFLLRGLQKTADFV 924
Db        635 --------------PQFAKYNRDVVLTEDGEH--------LEASRIPVQLR-------HV 665
```

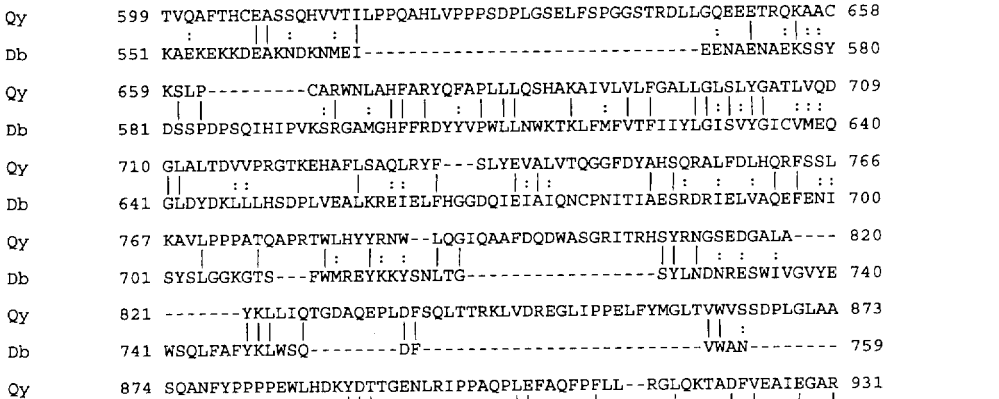


RESULT 13
T15830
hypothetical protein C54A12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15830
R;Bentley, D.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C54A12.
A;Reference number: Z18414
A;Accession: T15830
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1015 <BEN>
A;Cross-references: UNIPROT:Q09938; EMBL:U28733; NID:g861250; PID:g861251; PIDN:AAA68302
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C54A12.1
A;Introns: 33/3; 62/3; 110/3; 204/3; 233/2; 388/2; 413/1; 523/3; 604/2; 703/1; 792/1; 86

Query Match 6.9%; Score 430.5; DB 2; Length 1015;
Best Local Similarity 20.5%; Pred. No. 1.3e-21;
Matches 187; Conservative 153; Mismatches 339; Indels 233; Gaps 33;

RESULT 14
T29590
hypothetical protein F55F8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29590
R;Gattung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55F8.
A;Reference number: Z20647
A;Accession: T29590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-889 <GAT>
A;Cross-references: UNIPROT:P91346; EMBL:U80447; PIDN:AAB37812.1; GSPDB:GN00019; CESP:F5
A;Experimental source: strain Bristol N2; clone F55F8
C;Genetics:
A;Gene: CESP:F55F8.1
A;Map position: 1
A;Introns: 36/3; 66/3; 98/3; 149/2; 200/3; 240/2; 279/1; 358/1; 481/2; 569/3; 606/3; 697

Query Match 6.6%; Score 416.5; DB 2; Length 889;
Best Local Similarity 20.5%; Pred. No. 1e-20;
Matches 185; Conservative 153; Mismatches 355; Indels 211; Gaps 30;



```
Db        161 KLAKGDNGENIIVEA--TAWLLIYQLKFYPN---------------EISYVSGLWEREFK 203
Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTML------ 414
Db        204 NKMDEYKKQAKYISITYFHSQTLSDELNRNAERLAPKFIGAFVILVCFSVLCSIVTIKGS 263
Qy        415 -RWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFL 473
Db        264 GYIDWVVTKPILSVLGVSNAGMGIASAMGMLTYLEIQYNDIIA-VMPFLVVAVGTDNMFL 322
Qy        474 LAHAFTEALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533
Db        323 MVASLKRTDRNLKYDQRIAECMADAAVSILITALTDALSFGVGTITTIPAVQIFCIYTMC 382
Qy        534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGI 593
Db        383 ALLLTFAYQLTFFCAILVY---------------------------------------- 401
Qy        594 AHLTATVQAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPG------------G 640
Db        402 ---------YTRIEEQGLHSIWLRPAVTY---SSTSPLNVKLFWLGSQPQKPLPSCGTVS 449
Qy        641 STRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS 700
Db        450 STSSVSTMTSQATSPASKHLHHCA---ATSFFRNWYAPVLMQPWIRAIAGLWYLIYLGIS 506
Qy        701 LYGATLVQDGLALTDVV---PRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHS-QRAL 756
Db        507 IYGCTHLKEGLEPANLLVDDSYATPHYRVLEKHYWHYGA-SLQIVVSNPPDLRDPVERIN 565
Qy        757 FD-LHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSE 815
Db        566 MDKMASTFANCKVAIGDDSVQF----------WLREMQ-------VSEEIHKIQYDN--- 605
Qy        816 DGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQ 875
Db        606 -------------------------------------EKFYDHAAQYIYSD-----MSQ 622
Qy        876 ANFYPPPPEWLHD-KYDTTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAAC 934
Db        623 --------PWVVDVVWGRNNNSERI-----IKTFRFMIGMRDISTTTKQTEATNTFREIA 669
Qy        935 AEAGQAGVHAYPSGSP-FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIV 993
Db        670 SRFEQYNVTTY---MPLWLFTDQYALVVPNTMQDIIVAVACMLVISALLIPQPVCSFWVA 726
Qy        994 LVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGF-LTTQGSRNLRAA 1052
Db        727 VTIGSIDLGVLGFMTLWNVNLDAISMITIIMSVGFSVDYSAHITYAYVISKESTTSARVC 786
Qy       1053 HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF---FAALTVLTLLGLLHGLVLLPV 1109
Db        787 DALGDLGWPVAQGAMSTILAVSVLSDVPAYMIVTFFKTVFLAISI----GFLHGLVFLPL 842
Qy       1110 LLSI 1113
Db        843 MLSV 846
```

RESULT 15
T26521
hypothetical protein Y18D10A.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26521
R;Harris, B.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z20226
A;Accession: T26521
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-936 <WIL>
A;Cross-references: UNIPROT:Q9XW22; EMBL:AL034393; PIDN:CAA22312.1; CESP:Y18D10A.7
A;Experimental source: clone Y18D10A
C;Genetics:
A;Gene: CESP:Y18D10A.7
A;Introns: 11/1; 44/2; 106/1; 166/3; 289/2; 373/1; 396/3; 485/1; 573/3; 615/3; 644/3; 68

Query Match 6.2%; Score 389.5; DB 2; Length 936;
Best Local Similarity 20.1%; Pred. No. 8.4e-19;
Matches 186; Conservative 152; Mismatches 339; Indels 247; Gaps 33;

```
Qy        279 LSGGCHGFSHK--FMHWQEELLLGGMARDPQGELLR---AEALQSTFLLMSPRQLYEHFR 333
Db        149 LSSAGRIFTYKDVCLHFQNDCF-----SNPHAKLLANIYSKNHQNSMFNIT----YPIYR 199
Qy        334 GDYQTHDIGWSE-------------EQASTVL-------QAWQ--RRFVQ-LAQEALPEN 370
Db        200 STYATEPIDISKVLGNVSLDYDGHVENASAWLILYQLKNEKWQLSRDFEDGLAEKIQSGE 259
Qy        371 ASQQ---IHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVT--------------- 412
Db        260 APSELLNLYYFHSATFDQELEKENRRLTPKFSITPSVLIIFAIMTTFTIKFMKFKTENGI 319
Qy        413 ----MLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGV 468
Db        320 NQYPVIDW--VLSKPLLGICGVLVTMCAIISSTGLLMLFNVTFVDMCT-VMPFLSLTIGI 376
Qy        469 DDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFS 528
Db        377 DDTFLMLAAWHETDRNLPYEKRIEKAMRHAAVSISITSLTDALAFLIGSIAPLPAVIYFC 436
Qy        529 LQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT 588
Db        437 YYSSAAILFIFLYVLTMFVAVLALQGRREEDLKHSV------------------TGMKT 477
Qy        589 VPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQ 648
Db        478 IDLDSDYETASTR--------------------------------QLLLKMGSRVSVKAD 505
Qy        649 EEETRQK-----AACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYG 703
Db        506 EENNNNNNEKSIENIQKIDNRMW-YQRFFEDQYAPFISNSKISILSFLIYLAYLAAAFYG 564
Qy        704 ATLVQDG----------------LALTDVVPRGTKEHAFLSAQLRYF----SLYEVALVTQ 744
Db        565 VKHLKIGFDFVVTVVLTIKYKVLQLINIVQEDSASRVFLEVREQLFPEDTKLMDIAVMNS 624
Qy        745 GGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGR 804
Db        625 PNFSNPEER---FNFMEVLSEFESTWCSEGRESTQFWFFEMQKYLSNL--GFGGDLTK-- 677
Qy        805 ITRHSYRNGSEDGALAYKLLIQTG-----DAQEPLDFSQLTTRKLVDREGLIPPELFYMG 859
Db        678 -TMNSERKLSQ----SKKTFLMSHEKFGYDVLSDKQFRLSTRLKNVETD----EEMFNCA 728
Qy        860 LTVWVSSDPLGLAASQANF--YPPPPEW-LHDKYDTTGENLRIPPAQPLEFAQFPFLLRG 916
Db        729 RTM------RKLSQKHANYSIITYSPLWNIADEYD------------------------- 757
Qy        917 LQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTF 976
Db        758 ----------------------------------IMWPQTM---QDIYISIAVMVP--- 776
Qy        977 LVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHV 1036
Db        777 -VALLFIPQPLCSVIIGLNIASIAFGVIGTMSFLGVSLDATSMITVAMSVGFSVDFAAHV 835
Qy       1037 ALGFLTTQGSR-------NLRAAHALEHTFAPVTDGAISTLLGL--LMLAGSHFDFIVRY 1087
Db        836 SYAYMTESGAQIPGKSAIYSRFCHTLGTIGWPVTQASVSVLLGVSSLYLVDS---YVVQT 892
Qy       1088 FFAALTVLTLLGLLHGLVLLPVLL 1111
Db        893 CFRTVVLVILFGTTHALVFLPLLL 916
```

Search completed: November 22, 2004, 07:58:08
Job time : 32 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 10:37:41 ; Search time 914 Seconds
(without alignments)
7112.209 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09990046/runat_21112004_130921_18649/app_query.fasta_1.1351
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09990046_@CGN_1_1_511_@runat_21112004_130921_18649
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	6272	100.0	4030	9	US-09-990-046-1	Sequence 1, Appli
2	6248	99.6	4391	9	US-09-909-280A-1	Sequence 1, Appli
3	3955	63.1	4004	9	US-09-990-046-8	Sequence 8, Appli
4	3387	54.0	2082	9	US-09-990-046-9	Sequence 9, Appli
5	3349	53.4	5288	8	US-08-954-701A-18	Sequence 18, Appl
6	3349	53.4	5288	10	US-09-754-032-18	Sequence 18, Appl
7	3349	53.4	5288	15	US-10-421-446-18	Sequence 18, Appl
8	3337	53.2	5187	8	US-08-954-701A-3	Sequence 3, Appli
9	3337	53.2	5187	8	US-08-954-701A-9	Sequence 9, Appli
10	3337	53.2	5187	10	US-09-754-032-3	Sequence 3, Appli
11	3337	53.2	5187	10	US-09-754-032-9	Sequence 9, Appli
12	3337	53.2	5187	15	US-10-421-446-3	Sequence 3, Appli
13	3337	53.2	5187	15	US-10-421-446-9	Sequence 9, Appli
14	3336	53.2	6568	15	US-10-302-279-1	Sequence 1, Appli
15	3329	53.1	6568	9	US-09-964-824A-266	Sequence 266, App
16	1972.5	31.4	3900	8	US-08-954-771-42	Sequence 42, Appl
17	1972.5	31.4	3900	8	US-08-462-386D-42	Sequence 42, Appl
18	1972.5	31.4	3900	10	US-09-736-476-42	Sequence 42, Appl
19	1972.5	31.4	3900	18	US-10-647-654-42	Sequence 42, Appl
20	1956	31.2	4434	8	US-08-954-701A-5	Sequence 5, Appli
21	1956	31.2	4434	10	US-09-754-032-5	Sequence 5, Appli
22	1956	31.2	4434	15	US-10-421-446-5	Sequence 5, Appli
23	640	10.2	4550	14	US-10-208-731-1	Sequence 1, Appli
24	640	10.2	4673	15	US-10-172-118-459	Sequence 459, App
25	640	10.2	4673	16	US-10-342-887-459	Sequence 459, App
26	640	10.2	4673	17	US-10-776-827-100	Sequence 100, App
27	631	10.1	4814	10	US-09-971-392-103	Sequence 103, App
28	627	10.0	3996	16	US-10-621-758A-1	Sequence 1, Appli
29	627	10.0	3996	17	US-10-663-208A-1	Sequence 1, Appli
30	627	10.0	3996	17	US-10-646-301A-1	Sequence 1, Appli
31	627	10.0	3996	17	US-10-736-769-1	Sequence 1, Appli
32	627	10.0	4484	16	US-10-621-758A-9	Sequence 9, Appli
33	627	10.0	4484	17	US-10-663-208A-9	Sequence 9, Appli
34	627	10.0	4484	17	US-10-646-301A-9	Sequence 9, Appli
35	627	10.0	4484	17	US-10-736-769-9	Sequence 9, Appli
36	627	10.0	5092	16	US-10-621-758A-43	Sequence 43, Appl
37	627	10.0	5092	17	US-10-663-208A-43	Sequence 43, Appl
38	627	10.0	5092	17	US-10-646-301A-43	Sequence 43, Appl
39	627	10.0	5092	17	US-10-736-769-43	Sequence 43, Appl
40	615.5	9.8	3999	15	US-10-239-316-7	Sequence 7, Appli
41	609.5	9.7	3999	16	US-10-621-758A-3	Sequence 3, Appli
42	609.5	9.7	3999	17	US-10-663-208A-3	Sequence 3, Appli
43	609.5	9.7	3999	17	US-10-646-301A-3	Sequence 3, Appli
44	609.5	9.7	3999	17	US-10-736-769-3	Sequence 3, Appli
45	602.5	9.6	5029	14	US-10-208-731-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-990-046-1
; Sequence 1, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-046-1

Alignment Scores:

Pred. No.:	0	Length:	4030
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-990-046-1 (1-4030)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr  20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe  40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr  80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852

Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272

Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
```

```
Db      2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332

Qy       701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720

Db      2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392

Qy       721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740

Db      2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452

Qy       741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760

Db      2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512

Qy       761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780

Db      2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572

Qy       781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800

Db      2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632

Qy       801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820

Db      2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy       821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840

Db      2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752

Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860

Db      2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812

Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880

Db      2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872

Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900

Db      2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932

Qy       901 ProAlaGlnProLeuGluPheAlaGlnProProPheLeuLeuArgGlyLeuGlnLysThr 920

Db      2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940

Db      2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960

Db      3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980

Db      3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000

Db      3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020

Db      3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040

Db      3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060

Db      3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080

Db      3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100

Db      3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120

Db      3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140

Db      3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160

Db      3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180

Db      3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200

Db      3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy      1201 AlaThrGly 1203

Db      3833 GCCACTGGG 3841
```

RESULT 2
US-09-909-280A-1
; Sequence 1, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-909-280A-1

Alignment Scores:

Pred. No.:	0	Length:	4391
Score:	6248.00	Matches:	1200
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	9	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20

Db        297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356
```

```
Qy       21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db      357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy       41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db      417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy       61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db      477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy       81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db      537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy      101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db      597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656

Qy      121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db      657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716

Qy      141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db      717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776

Qy      161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db      777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836

Qy      181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db      837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896

Qy      201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db      897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956

Qy      221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db      957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016

Qy      241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db     1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076

Qy      261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db     1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136

Qy      281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db     1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196

Qy      301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db     1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256

Qy      321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db     1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316

Qy      341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db     1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376

Qy      361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db     1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436

Qy      381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db     1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496

Qy      401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db     1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556

Qy      421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db     1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616

Qy      441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db     1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676

Qy      461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db     1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736

Qy      481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db     1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796

Qy      501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db     1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856

Qy      521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db     1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916

Qy      541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db     1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976

Qy      561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db     1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036

Qy      581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db     2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096

Qy      601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db     2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156

Qy      621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db     2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216

Qy      641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db     2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276

Qy      661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db     2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336

Qy      681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db     2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396

Qy      701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db     2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456

Qy      721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db     2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516

Qy      741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
```

```
Db       2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576

Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780

Db       2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800

Db       2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820

Db       2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840

Db       2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860

Db       2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880

Db       2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900

Db       2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996

Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920

Db       2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940

Db       3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960

Db       3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980

Db       3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000

Db       3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020

Db       3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040

Db       3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060

Db       3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080

Db       3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100

Db       3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120

Db       3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140

Db       3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160

Db       3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180

Db       3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200

Db       3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy       1201 AlaThrGly 1203

Db       3897 GCCACTGGG 3905
```

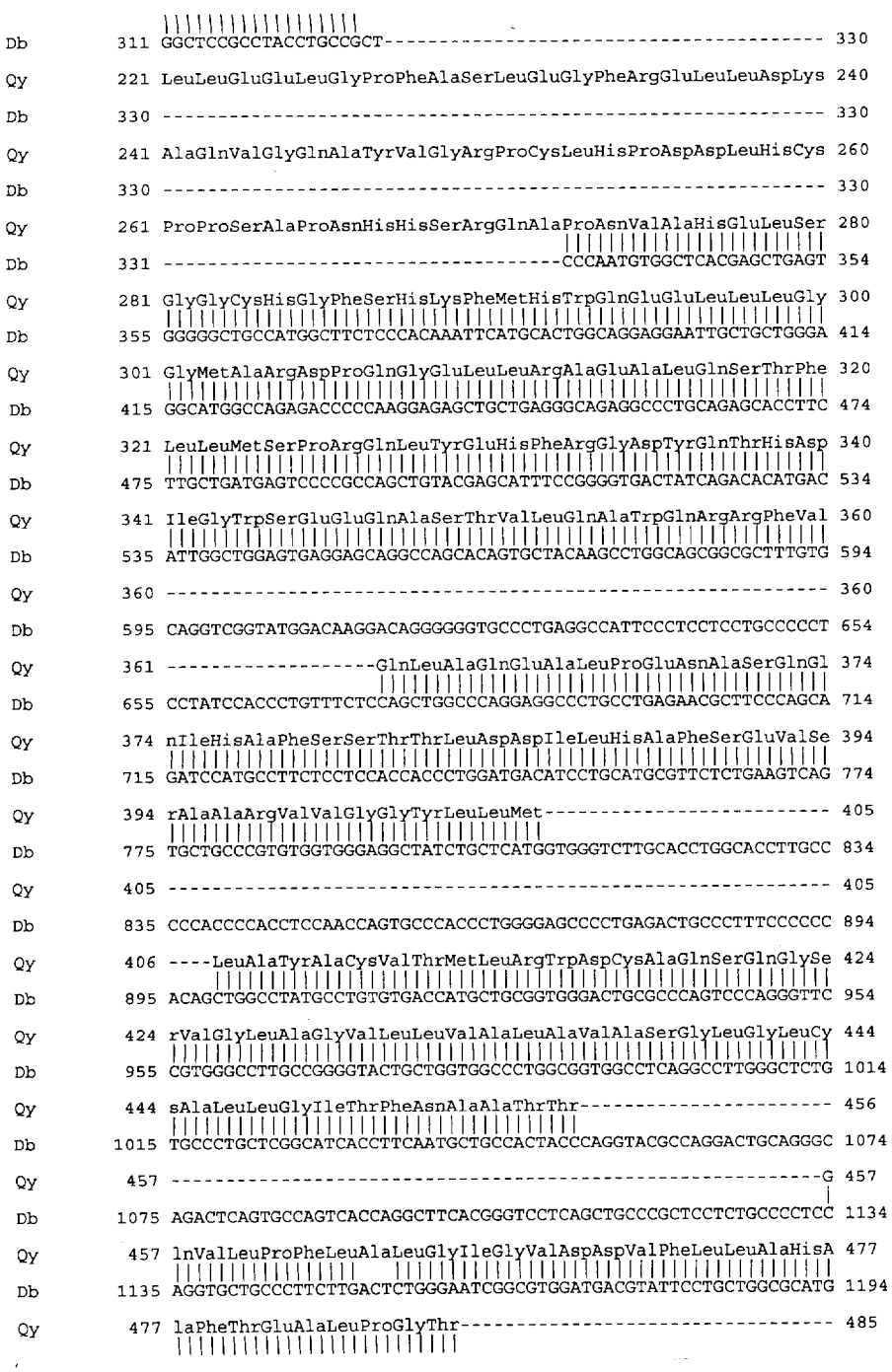
RESULT 3
US-09-990-046-8
; Sequence 8, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 8
; LENGTH: 4004
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-046-8

Alignment Scores:

Pred. No.:	0	Length:	4004
Score:	3955.00	Matches:	847
Percent Similarity:	65.81%	Conservative:	2
Best Local Similarity:	65.66%	Mismatches:	10
Query Match:	63.06%	Indels:	434
DB:	9	Gaps:	10

US-09-990-046-2 (1-1203) x US-09-990-046-8 (1-4004)

```
Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120

Db         11 CGGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 70

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140

Db         71 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 130

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160

Db        131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 190

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180

Db        191 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200

Db        251 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 310

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
```

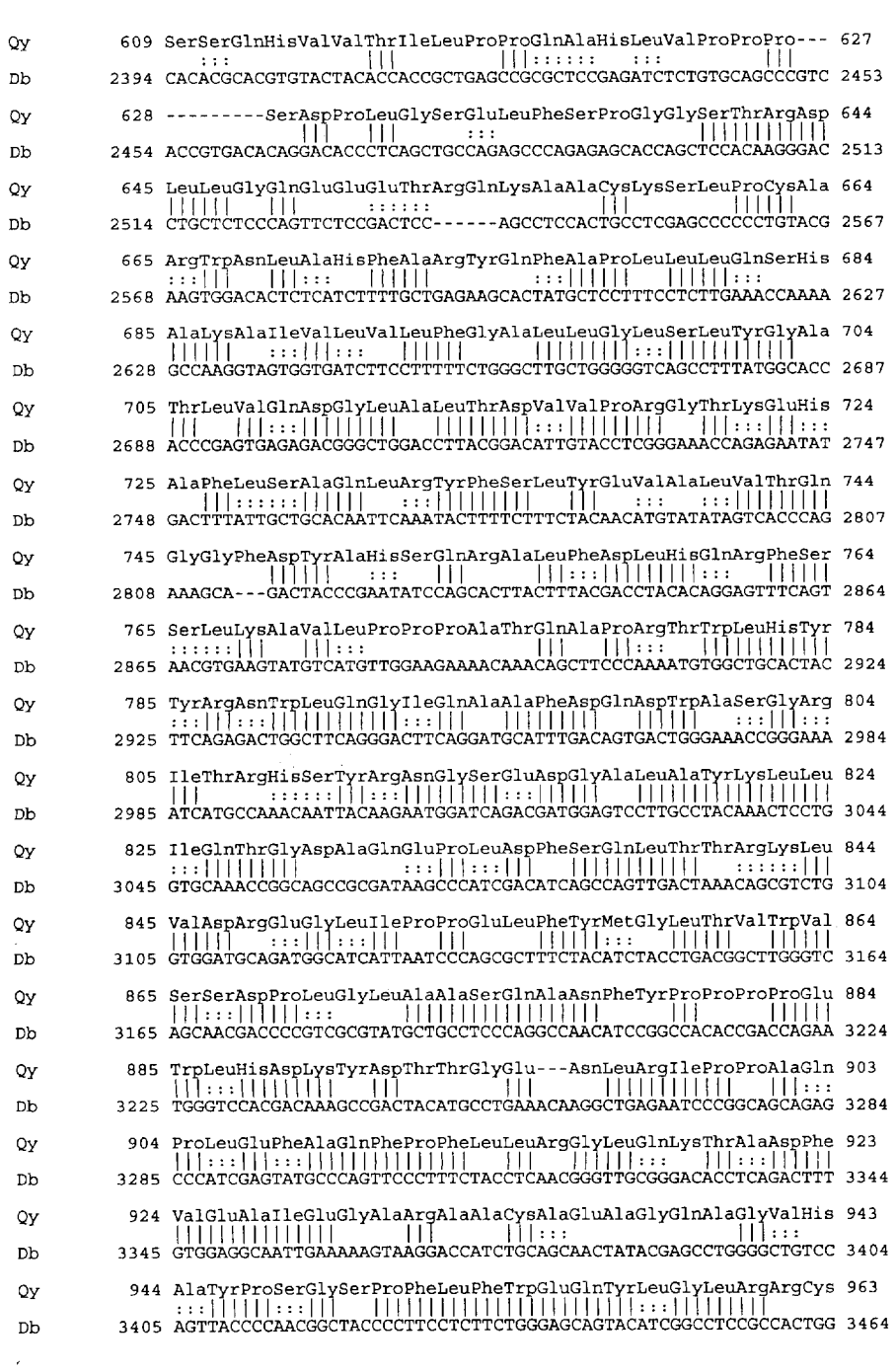

Db 311 GGCTCCGCCTACCTGCCGCT 330
Qy 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 330 330
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 330 330
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 331 CCCAATGTGGCTCACGAGCTGAGT 354
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 355 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 594
Qy 360 360
Db 595 CAGGTCGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 654
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGl 374
Db 655 CCTATCCACCCTGTTTCTCCAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet 405
Db 775 TGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGTGGGTCTTGCACCTGGCACCTTGCC 834
Qy 405 405
Db 835 CCCACCCCACCTCCAACCAGTGCCCACCCTGGGGAGCCCCTGAGACTGCCCTTTCCCCCC 894
Qy 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 G 457
Db 1075 AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTGCTGCCCTTCTTGACTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr 485
Db 1195 CCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254
Qy 485 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 485
Db 1315 ATGAACCTCGGTGCCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGCTGTGTCCT 1374
Qy 485 485
Db 1375 AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 485
Db 1435 ACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 485
Db 1495 CAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGAGG 1554
Qy 486 ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCCACTCTGTCCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTTGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTC 1673
Qy 520 roIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC 1699
Qy 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys 559
Db 1700 CTACAGCCTGGACCTACGGCGGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCCTGCGCCCCAGCCCCTTCCT 1789
Qy 569 569
Db 1790 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 1849
Qy 570 SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269

```
Qy       705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db      2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329

Qy       725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db      2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389

Qy       745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db      2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449

Qy       765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db      2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509

Qy       785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db      2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569

Qy       805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db      2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629

Qy       825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------------------- 837
Db      2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689

Qy       837 ------------------------------------------------------------ 837
Db      2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749

Qy       838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
Db      2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809

Qy       857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
Db      2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869

Qy       877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
Db      2870 AACTTCTACCCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929

Qy       897 LeuArg-------------------------------------------------------- 898
Db      2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989

Qy       898 ------------------------------------------------------------ 898
Db      2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049

Qy       899 ------------------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db      3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109

Qy       912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db      3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169

Qy       932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db      3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229

Qy       952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db      3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289

Qy       972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
Db      3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349

Qy       992 e------------------------------------------------------------ 992
Db      3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

Qy       993 ----------------------------------------ValLeuValLeuAlaMetM 999
Db      3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy       999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
Db      3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529

Qy      1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
Db      3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy      1039 lyPheLeuThrThrGlnGly 1045
Db      3590 TGAGCACGGGCACCCCGGGG 3609

RESULT 4
US-09-990-046-9
; Sequence 9, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
;  APPLICANT: de Sauvage, Frederic
;  APPLICANT:  Carpenter, David A.
;  TITLE OF INVENTION: Patched-2
;  FILE REFERENCE: P1405R1
;  CURRENT APPLICATION NUMBER: US/09/990,046
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 9
;   LENGTH: 2082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-990-046-9

Alignment Scores:
Pred. No.:                3.35e-308      Length:          2082
Score:                    3387.00        Matches:         656
Percent Similarity:       96.33%         Conservative:    1
Best Local Similarity:    96.19%         Mismatches:      3
Query Match:              54.00%         Indels:          23
DB:                       9              Gaps:            2

US-09-990-046-2 (1-1203) x US-09-990-046-9 (1-2082)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db          8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db         68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db        128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db        188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db        248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db        308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367
```

```
Qy       121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db       368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy       141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db       428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy       161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db       488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547

Qy       181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db       548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy       201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db       608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy       221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db       668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy       241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db       728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy       261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy       281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907

Qy       301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy       321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db      1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db      1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy       541 AlaValMetLeuValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT--------------TTCGCCCCGGAATTC 1980

Qy       681 LeuGln 682
Db      1981 CTGCAG 1986
```

RESULT 5
US-08-954-701A-18
; Sequence 18, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709

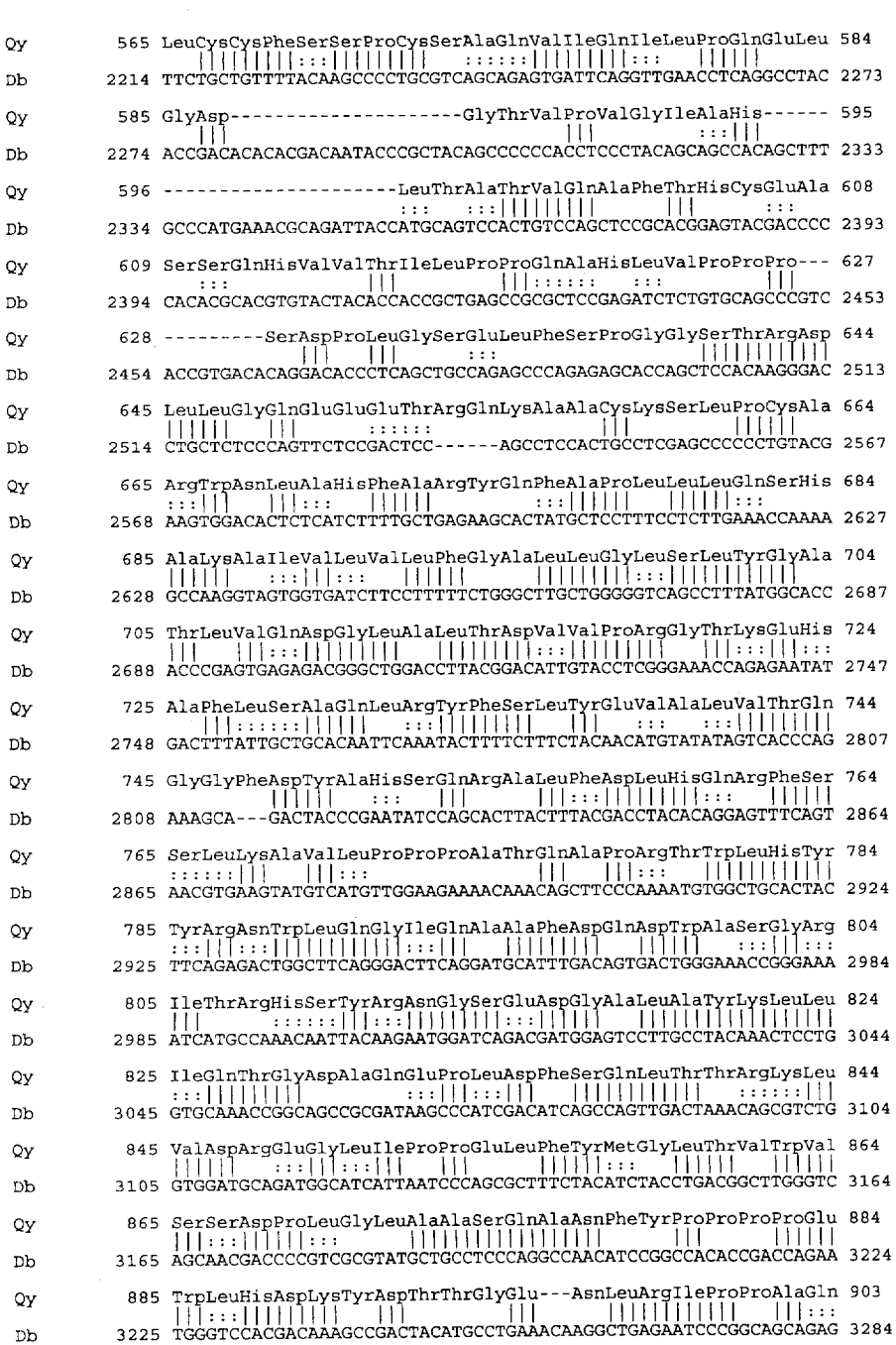
```
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-954-701A-18

Alignment Scores:
Pred. No.:                4.8e-304      Length:          5288
Score:                    3349.00       Matches:         662
Percent Similarity:       70.02%        Conservative:    200
Best Local Similarity:    53.78%        Mismatches:      298
Query Match:              53.40%        Indels:          71
DB:                       8             Gaps:            16

US-09-990-046-2 (1-1203) x US-08-954-701A-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db       1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy        427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db       1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy        447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db       1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy        467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db       1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973

Qy        485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db       1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033

Qy        505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db       2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093

Qy        525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db       2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153

Qy        545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db       2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213

Qy        565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db       2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273

Qy        585 GlyAsp--------------------GlyThrValProValGlyIleAlaHis------ 595
Db       2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333

Qy        596 --------------------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db       2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
```



RESULT 6
US-09-754-032-18
; Sequence 18, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

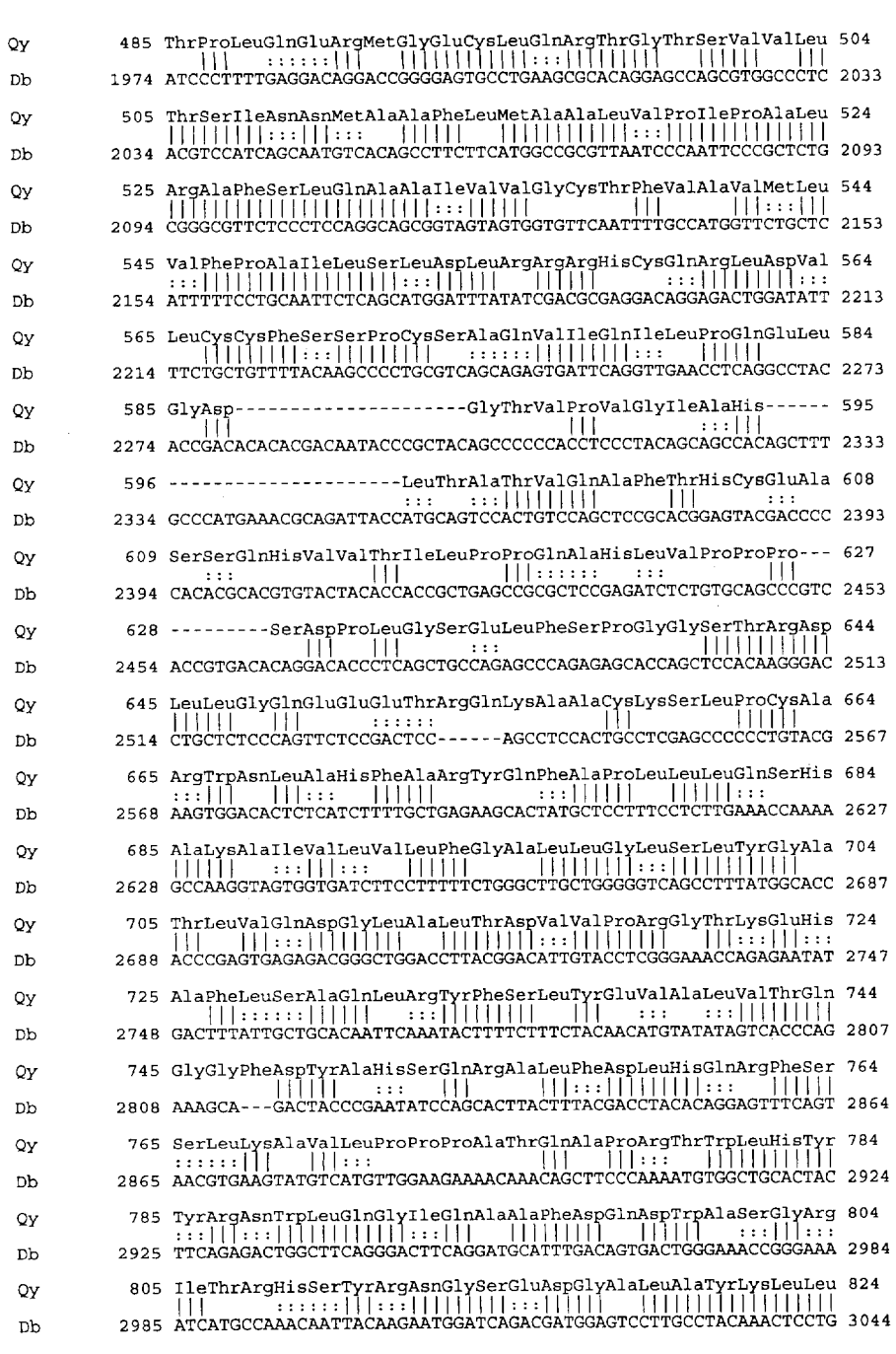
```
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/754,032
;           FILING DATE: 03-Jan-2001
;           CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/540,406
;           FILING DATE: 06-OCT-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Rowland, Bertram I
;           REGISTRATION NUMBER: 20015
;           REFERENCE/DOCKET NUMBER: a60190-1
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 415-781-1989
;           TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 5288 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-754-032-18

Alignment Scores:
Pred. No.:                  4.8e-304        Length:          5288
Score:                      3349.00         Matches:         662
Percent Similarity:         70.02%          Conservative:    200
Best Local Similarity:      53.78%          Mismatches:      298
Query Match:                53.40%          Indels:          71
DB:                         10              Gaps:            16

US-09-990-046-2 (1-1203) x US-09-754-032-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
```

```
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db       1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy        427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db       1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy        447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db       1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy        467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db       1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973

Qy        485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db       1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033

Qy        505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db       2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093

Qy        525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db       2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153

Qy        545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db       2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
```

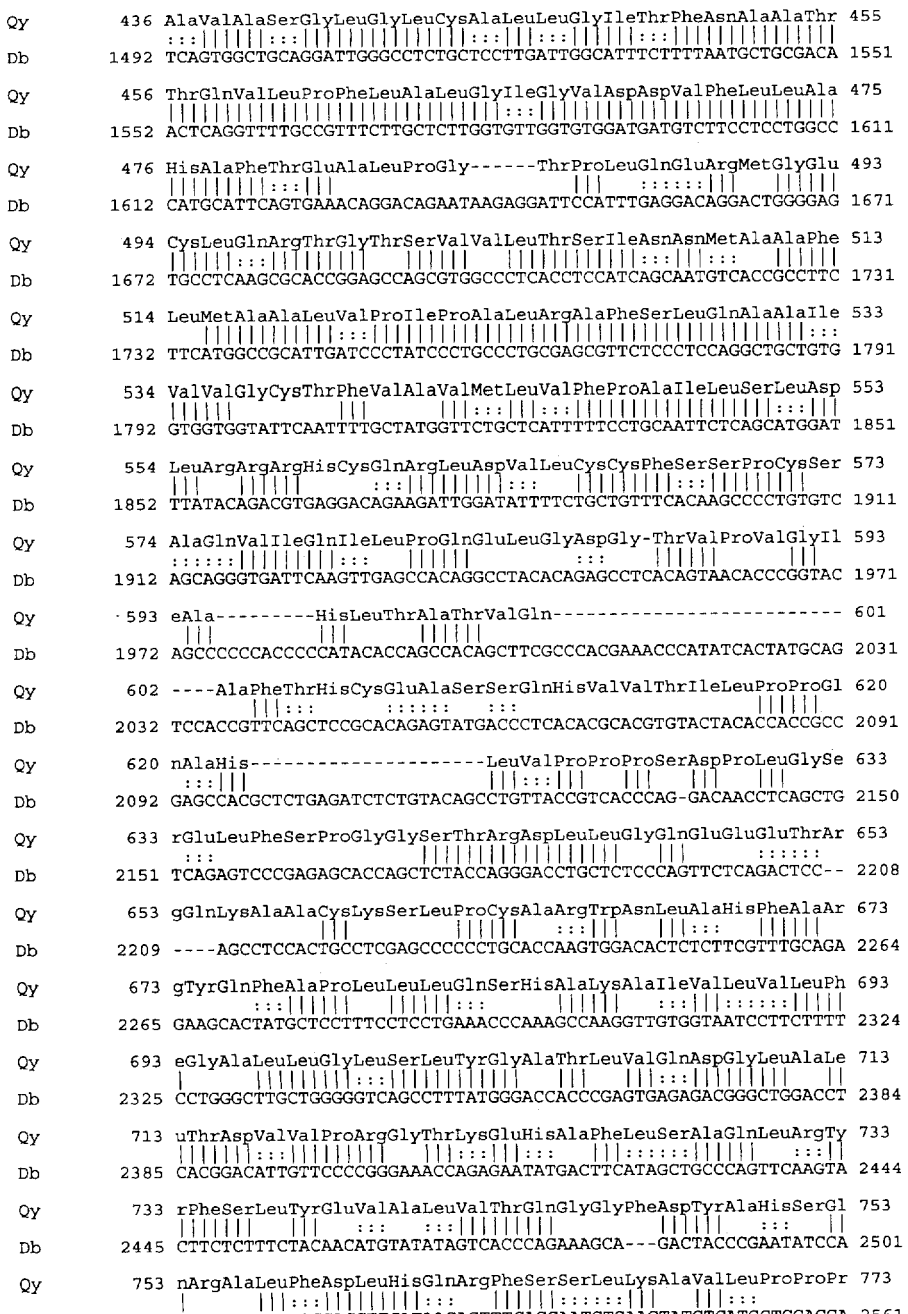


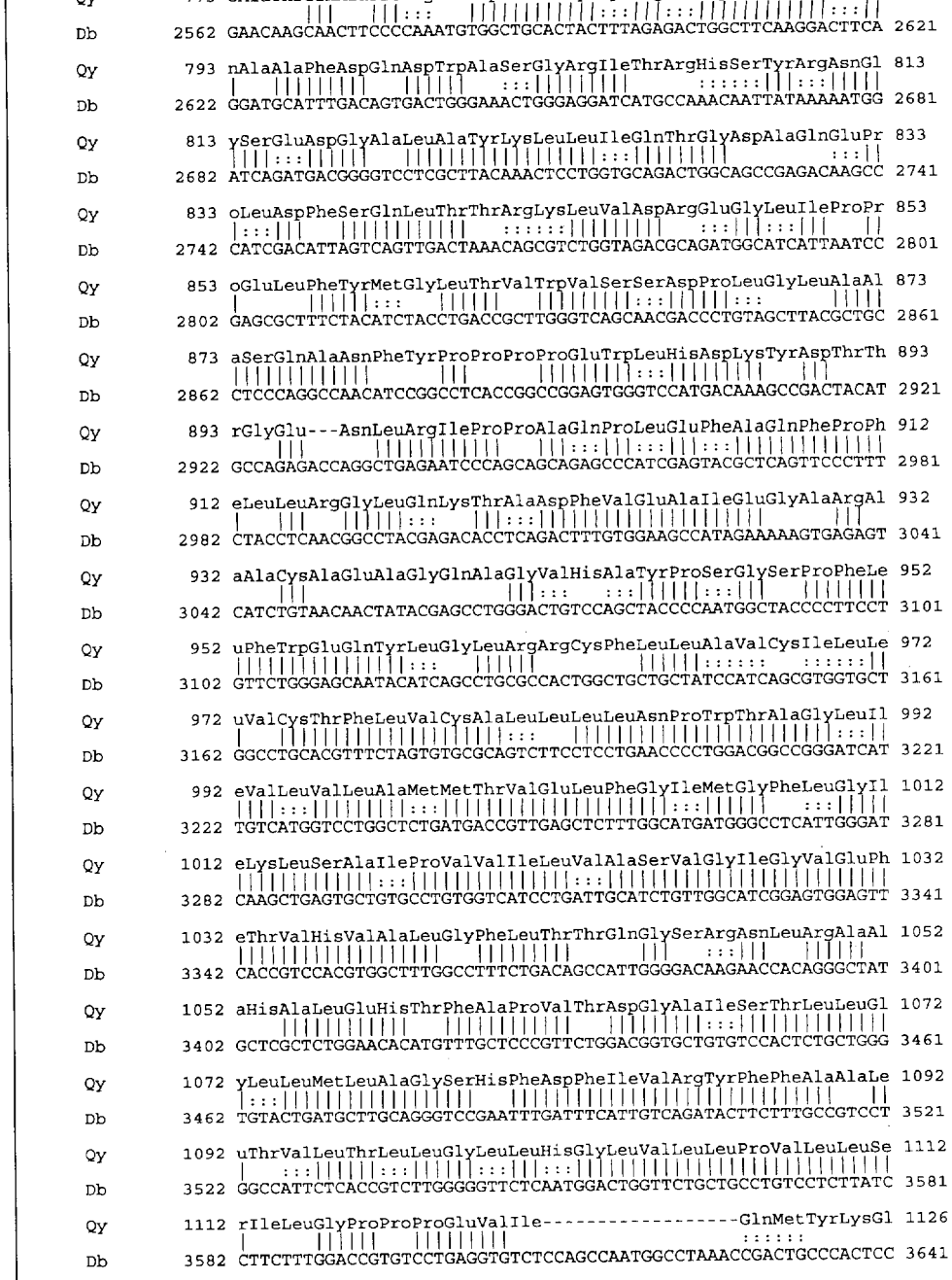
RESULT 7
US-10-421-446-18
; Sequence 18, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use

```
;       NUMBER OF SEQUENCES: 19
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;            STREET: Four Embarcadero Center, Suite 3400
;            CITY: San Francisco
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/421,446
;            FILING DATE: 22-Apr-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/724,631
;            FILING DATE: 28-No. US20030186309A1-2000
;            APPLICATION NUMBER: US/08/656,055
;            FILING DATE: 1996-05-31
;            APPLICATION NUMBER: 08/540,406
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Rowland, Bertram I
;            REGISTRATION NUMBER: 20015
;            REFERENCE/DOCKET NUMBER: a60190-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-781-1989
;            TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5288 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-421-446-18

Alignment Scores:
Pred. No.:                4.8e-304      Length:          5288
Score:                    3349.00       Matches:         662
Percent Similarity:       70.02%        Conservative:    200
Best Local Similarity:    53.78%        Mismatches:      298
Query Match:              53.40%        Indels:          71
DB:                       15            Gaps:            16

US-09-990-046-2 (1-1203) x US-10-421-446-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
              |||||||||       |||      |||       ||||||      |||
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
                   ||||||||||||||||||||||||  ||||||  |||||||||  ||||||
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
              |||   ||||||::::::|||||||||   |||   :::|||||||||  |||||||||
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
                 |||:::|||||:::   |||   :::||||||||:::|||:::|||||||||||||
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
              ||||||   |||||||||:::|||||||::||||||::::::|||:::||||||||||||
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
                 :::      |||::::::||||||||||   ::::::||||||   |||:::||||||

Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
              |||||||||       ||||||   :::||||||   ||||||:::|||   |||
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
                 :::|||   :::   |||   |||      :::|||||||||||||||      :::
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrPro 188
              |||   |||   ::::::   :::||||||   |||:::|||||:::|||:::||||||
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
              ||||||||||||||||||||||||||||||   |||:::|||||||||   |||:::
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
              |||   ::::::|||||||||   ||||||   :::   ||||||||||||
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
                    ::::::   :::   |||:::|||:::||||||:::||||||      |||
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
              :::   |||||||||||||:::|||   |||      ||||||   :::|||||||||
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
              :::|||   :::      ::::::|||      |||:::|||||||||||||||   |||
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
                 |||:::|||||||||||||||||||||||:::::||||||      ::::::
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
              |||:::|||:::   |||   |||||||||:::   |||   ||||||:::|||:::|||
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
              :::|||||||||||||:::|||   :::|||   :::|||   |||   |||:::|||:::
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
              :::|||:::   :::|||:::||||||||||||   :::|||::::::      ::::::
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
              :::   :::|||::::::|||::::::   :::|||::::::||||||||||||||||||
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
              |||   :::||||||:::||||||      ||||||      ||||||||||||||||||
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
              ||||||||||:::||||||||||||||||||||||::::::||||||||:::||||||
Db       1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy        427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
              ||||||||||||||||||||||||:::||||||:::||||||||||||||||:::|||
Db       1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy        447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
              :::||||||:::||||||||||||||||||||||||||||||||||||||||||||:::
Db       1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy        467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
              |||||||||||||||||||||||||||||||||||||||||:::|||
Db       1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
```

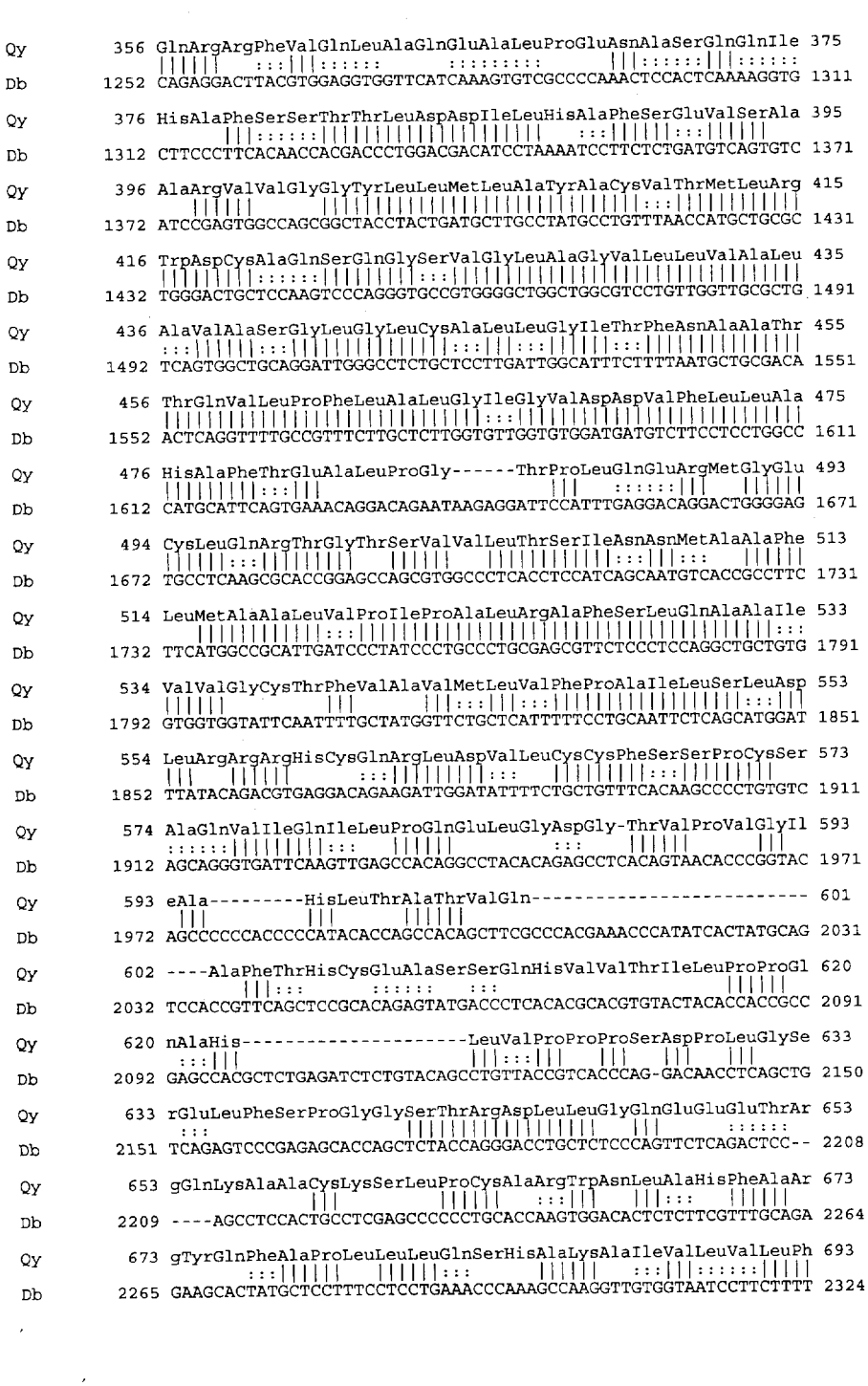

Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
Qy 944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464
Qy 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524
Qy 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584
Qy 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db 3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644
Qy 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db 3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704
Qy 1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db 3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764
Qy 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db 3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824
Qy 1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db 3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884
Qy 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTGGACCATATCCTGAGGTGTCTCCAGCC 3944
Qy 1123 tTyrLys----------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db 3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG---------- 3993
Qy 1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db 3994 ----------TGGTCCGCTTCGCCATGCCGCCCG----------GCCAC 4022
Qy 1159 rMetThrValAlaIleHisProPro---------- 1167
Db 4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082
Qy 1168 ----------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180

```
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173

RESULT 8
US-08-954-701A-3
; Sequence 3, Application US/08954701A
; Publication No. US20030032085A1
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,701A
;      FILING DATE:  20-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36709
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5187 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-954-701A-3

Alignment Scores:
Pred. No.:                6.28e-303      Length:          5187
Score:                    3337.00        Matches:         677
Percent Similarity:       69.59%         Conservative:    204
Best Local Similarity:    53.48%         Mismatches:      306
Query Match:              53.20%         Indels:          80
DB:                       8              Gaps:            20

US-09-990-046-2 (1-1203) x US-08-954-701A-3 (1-5187)

Qy          3 ArgSerProProLeuArgGluLeu------ProProSerTyrThrProProAlaArgThr 20
Db        178 CGCGCCGCGCCGGACCGGGACTATCTGCACCGGCCCAGCTACTGC---GACGCCGCCTTC 234

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeu---------LysAlaProLeuTrpLeuArg 37
Db        235 GCTCTGGAGCAGATTTCCAAGGGGAAGGCTACTGGCCGGAAAGCGCCGCTGTGGCTGAGA 294

Qy         38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db        295 GCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTACATTCAAAAGAACTGCGGCAAG 354

Qy         58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77

Db        355 TTTTTGGTTGTGGGTCTCCTCATATTTGGGGCCTTCGCTGTGGGATTAAAGGCAGCTAAT 414

Qy         78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
Db        415 CTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGTGGACGAGTGAGTCGAGAATTA 474

Qy         98 HisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
Db        475 AATTATACCCGTCAGAAGATAGGAGAAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534

Qy        118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137
Db        535 ACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACAGAGGCTCTCCTGCAACACCTGGAC 594

Qy        138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
Db        595 TCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATGTATAACAGGCAATGGAAGTTGGAA 654

Qy        158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
Db        655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714

Qy        178 GluLysLeuProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
Db        715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774

Qy        198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
Db        775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834

Qy        218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db        835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894

Qy        237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db        895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954

Qy        257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
Db        955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014

Qy        277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296
Db       1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074

Qy        297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316
Db       1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134

Qy        317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
Db       1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194

Qy        336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db       1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251

Qy        356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
Db       1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311

Qy        376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
Db       1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371

Qy        396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
Db       1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431

Qy        416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
Db       1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491
```



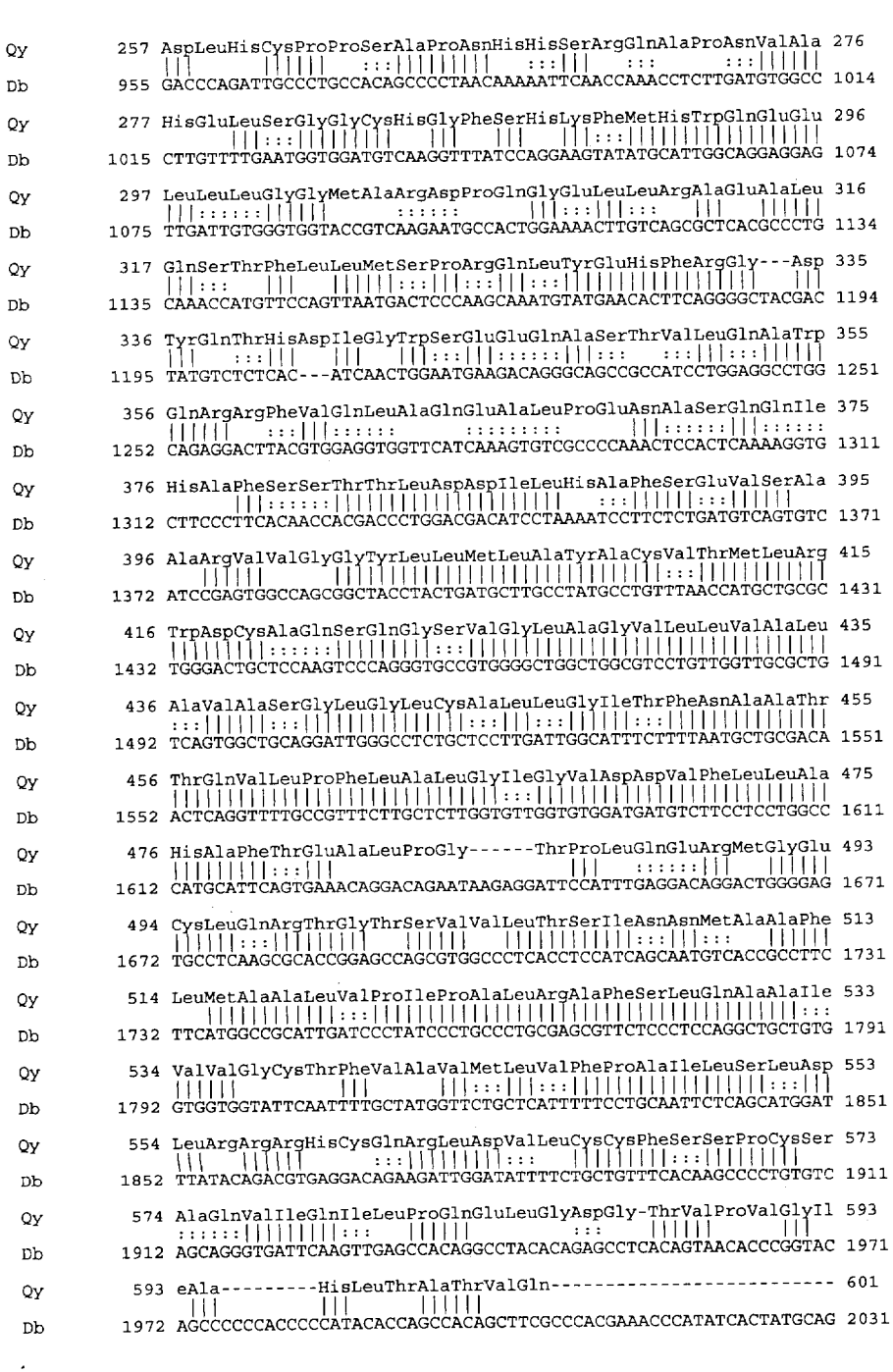


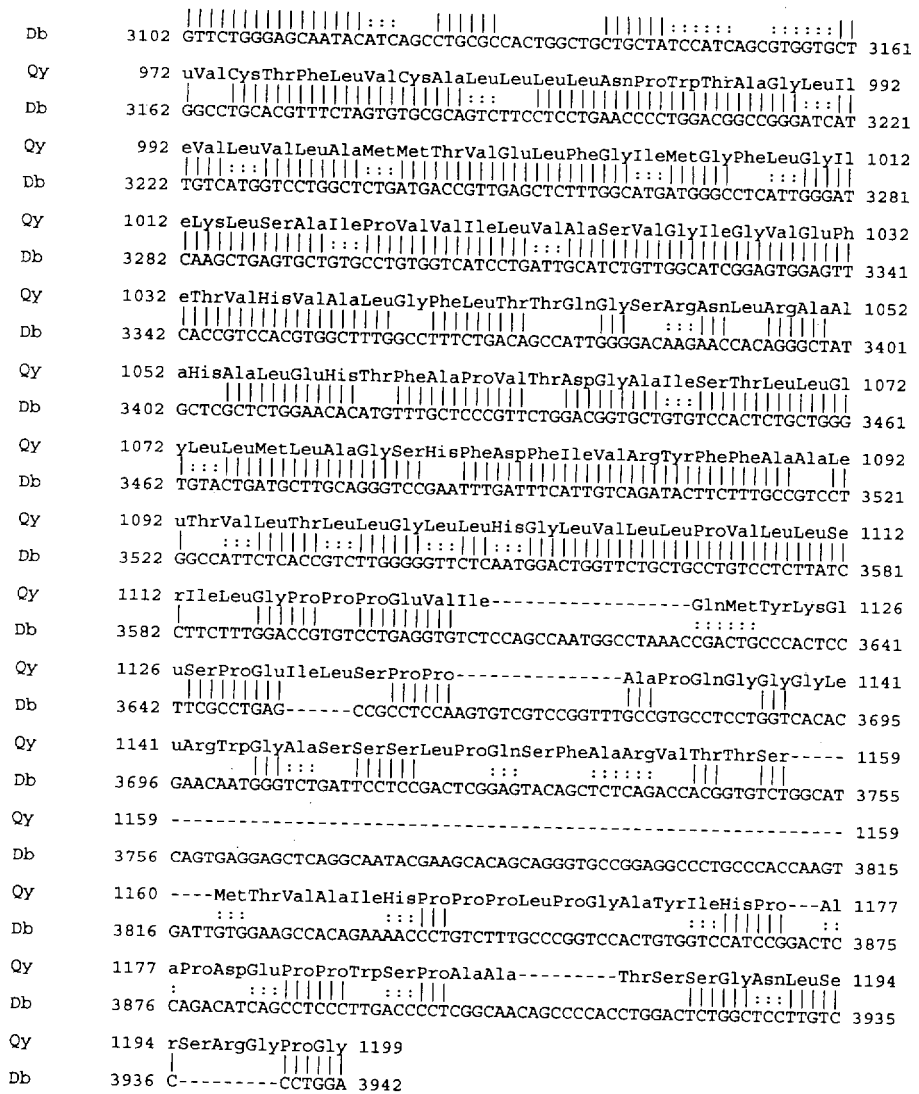
```
Db       3642 TTCGCCTGAG------CCGCCTCCAAGTGTCGTCCGGTTTGCCGTGCCTCCTGGTCACAC 3695

Qy       1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159

Db       3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755

Qy       1159 ------------------------------------------------------------ 1159

Db       3756 CAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGGTGCCGGAGGCCCTGCCCACCAAGT 3815

Qy       1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177

Db       3816 GATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCGGTCCACTGTGGTCCATCCGGACTC 3875

Qy       1177 aProAspGluProProTrpSerProAlaAla---------ThrSerSerGlyAsnLeuSe 1194

Db       3876 CAGACATCAGCCTCCCTTGACCCCTCGGCAACAGCCCCACCTGGACTCTGGCTCCTTGTC 3935

Qy       1194 rSerArgGlyProGly 1199

Db       3936 C---------CCTGGA 3942

RESULT 9
US-08-954-701A-9
; Sequence 9, Application US/08954701A
; Publication No. US20030032085A1
;  GENERAL INFORMATION:
;     APPLICANT:  SCOTT, MATHEW P
;     APPLICANT:  GOODRICH, LISA V
;     APPLICANT:  JOHNSON, RONALD L
;     TITLE OF INVENTION:  Patched Genes and their Use
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley, Hoag & Eliot
;       STREET:  One Post Office Square
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII(text)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/954,701A
;       FILING DATE:  20-OCT-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Vincent, Matthew P.
;       REGISTRATION NUMBER:  36709
;       REFERENCE/DOCKET NUMBER:  SUV-003.08
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-832-1000
;       TELEFAX:  617-832-7000
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5187 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-954-701A-9

Alignment Scores:
Pred. No.:                6.28e-303      Length:          5187
Score:                    3337.00        Matches:          677
Percent Similarity:       69.59%         Conservative:     204
Best Local Similarity:    53.48%         Mismatches:       306
Query Match:              53.20%         Indels:            80
DB:                       8              Gaps:              20

US-09-990-046-2 (1-1203) x US-08-954-701A-9 (1-5187)

Qy          3 ArgSerProProLeuArgGluLeu------ProProSerTyrThrProProAlaArgThr 20

Db        178 CGCGCCGCGCCGGACCGGGACTATCTGCACCGGCCCAGCTACTGC---GACGCCGCCTTC 234

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeu---------LysAlaProLeuTrpLeuArg 37

Db        235 GCTCTGGAGCAGATTTCCAAGGGGAAGGCTACTGGCCGGAAAGCGCCGCTGTGGCTGAGA 294

Qy         38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57

Db        295 GCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTACATTCAAAAGAACTGCGGCAAG 354

Qy         58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77

Db        355 TTTTTGGTTGTGGGTCTCCTCATATTTGGGGCCTTCGCTGTGGGATTAAAGGCAGCTAAT 414

Qy         78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97

Db        415 CTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGTGGACGAGTGAGTCGAGAATTA 474

Qy         98 HisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117

Db        475 AATTATACCCGTCAGAAGATAGGAGAAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534

Qy        118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137

Db        535 ACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACAGAGGCTCTCCTGCAACACCTGGAC 594

Qy        138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157

Db        595 TCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATGTATAACAGGCAATGGAAGTTGGAA 654

Qy        158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177

Db        655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714

Qy        178 GluLysLeuProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197

Db        715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774

Qy        198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217

Db        775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834

Qy        218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236

Db        835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894

Qy        237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256

Db        895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954

Qy        257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276

Db        955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014

Qy        277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296

Db       1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074

Qy        297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316

Db       1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134

Qy        317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335

Db       1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194

Qy        336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355

Db       1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251
```


Qy 356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
Db 1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311
Qy 376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
Db 1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371
Qy 396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
Db 1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431
Qy 416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
Db 1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491
Qy 436 AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr 455
Db 1492 TCAGTGGCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACA 1551
Qy 456 ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla 475
Db 1552 ACTCAGGTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCC 1611
Qy 476 HisAlaPheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGlu 493
Db 1612 CATGCATTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAG 1671
Qy 494 CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe 513
Db 1672 TGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTC 1731
Qy 514 LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
Db 1732 TTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 1791
Qy 534 ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp 553
Db 1792 GTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATTTTTCCTGCAATTCTCAGCATGGAT 1851
Qy 554 LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer 573
Db 1852 TTATACAGACGTGAGGACAGAAGATTGGATATTTTCTGCTGTTTCACAAGCCCCTGTGTC 1911
Qy 574 AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIl 593
Db 1912 AGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACAGAGCCTCACAGTAACACCCGGTAC 1971
Qy 593 eAla---------HisLeuThrAlaThrValGln---------- 601
Db 1972 AGCCCCCCACCCCCATACACCAGCCACAGCTTCGCCCACGAAACCCATATCACTATGCAG 2031
Qy 602 ----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
Db 2032 TCCACCGTTCAGCTCCGCACAGAGTATGACCCTCACACGCACGTGTACTACACCACCGCC 2091
Qy 620 nAlaHis--------------------LeuValProProProSerAspProLeuGlySe 633
Db 2092 GAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACCGTCACCCAG-GACAACCTCAGCTG 2150
Qy 633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThrAr 653
Db 2151 TCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCTGCTCTCCCAGTTCTCAGACTCC-- 2208
Qy 653 gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db 2209 ----AGCCTCCACTGCCTCGAGCCCCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA 2264
Qy 673 gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh 693
Db 2265 GAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGCCAAGGTTGTGGTAATCCTTCTTTT 2324
Qy 693 eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db 2325 CCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACCCGAGTGAGAGACGGGCTGGACCT 2384
Qy 713 uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db 2385 CACGGACATTGTTCCCCGGGAAACCAGAGAATATGACTTCATAGCTGCCCAGTTCAAGTA 2444
Qy 733 rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db 2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA---GACTACCCGAATATCCA 2501
Qy 753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
Db 2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561
Qy 773 oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGl 793
Db 2562 GAACAAGCAACTTCCCCAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
Qy 793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813
Db 2622 GGATGCATTTGACAGTGACTGGGAAACTGGGAGGATCATGCCAAACAATTATAAAAATGG 2681
Qy 813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
Db 2682 ATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGTGCAGACTGGCAGCCGAGACAAGCC 2741
Qy 833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853
Db 2742 CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGCAGATGGCATCATTAATCC 2801
Qy 853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
Db 2802 GAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGACCCTGTAGCTTACGCTGC 2861
Qy 873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893
Db 2862 CTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCATGACAAAGCCGACTACAT 2921
Qy 893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db 2922 GCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCCTTT 2981
Qy 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db 2982 CTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAAGTGAGAGT 3041
Qy 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db 3042 CATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTTCCT 3101
Qy 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db 3102 GTTCTGGGAGCAATACATCAGCCTGCGCCACTGGCTGCTGCTATCCATCAGCGTGGTGCT 3161
Qy 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
Db 3162 GGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCTGAACCCCTGGACGGCCGGGATCAT 3221
Qy 992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl 1012
Db 3222 TGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCCTCATTGGGAT 3281
Qy 1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032
Db 3282 CAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGCATCTGTTGGCATCGGAGTGGAGTT 3341
Qy 1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
Db 3342 CACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCATTGGGGACAAGAACCACAGGGCTAT 3401
Qy 1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072

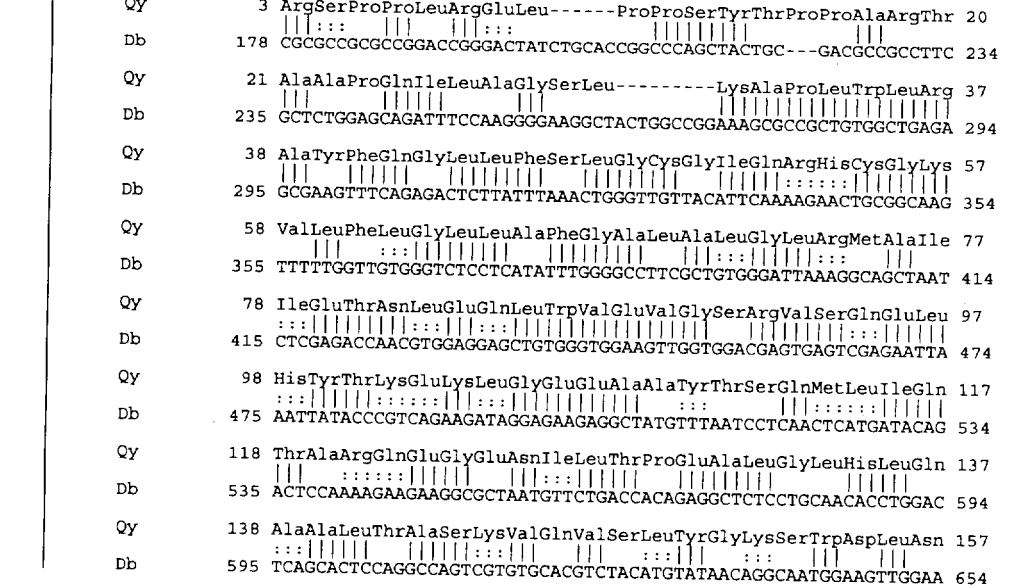
```
Db       3402 GCTCGCTCTGGAACACATGTTTGCTCCCGTTCTGGACGGTGCTGTGTCCACTCTGCTGGG 3461

Qy       1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092

Db       3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTCAGATACTTCTTTGCCGTCCT 3521

Qy       1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

Db       3522 GGCCATTCTCACCGTCTTGGGGGTTCTCAATGGACTGGTTCTGCTGCCTGTCCTCTTATC 3581

Qy       1112 rIleLeuGlyProProProGluValIle----------------GlnMetTyrLysGl 1126

Db       3582 CTTCTTTGGACCGTGTCCTGAGGTGTCTCCAGCCAATGGCCTAAACCGACTGCCCACTCC 3641

Qy       1126 uSerProGluIleLeuSerProPro--------------AlaProGlnGlyGlyGlyLe 1141

Db       3642 TTCGCCTGAG------CCGCCTCCAAGTGTCGTCCGGTTTGCCGTGCCTCCTGGTCACAC 3695

Qy       1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159

Db       3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755

Qy       1159 ------------------------------------------------------------ 1159

Db       3756 CAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGGTGCCGGAGGCCCTGCCCACCAAGT 3815

Qy       1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177

Db       3816 GATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCGGTCCACTGTGGTCCATCCGGACTC 3875

Qy       1177 aProAspGluProProTrpSerProAlaAla---------ThrSerSerGlyAsnLeuSe 1194

Db       3876 CAGACATCAGCCTCCCTTGACCCCTCGGCAACAGCCCCACCTGGACTCTGGCTCCTTGTC 3935

Qy       1194 rSerArgGlyProGly 1199

Db       3936 C---------CCTGGA 3942
```

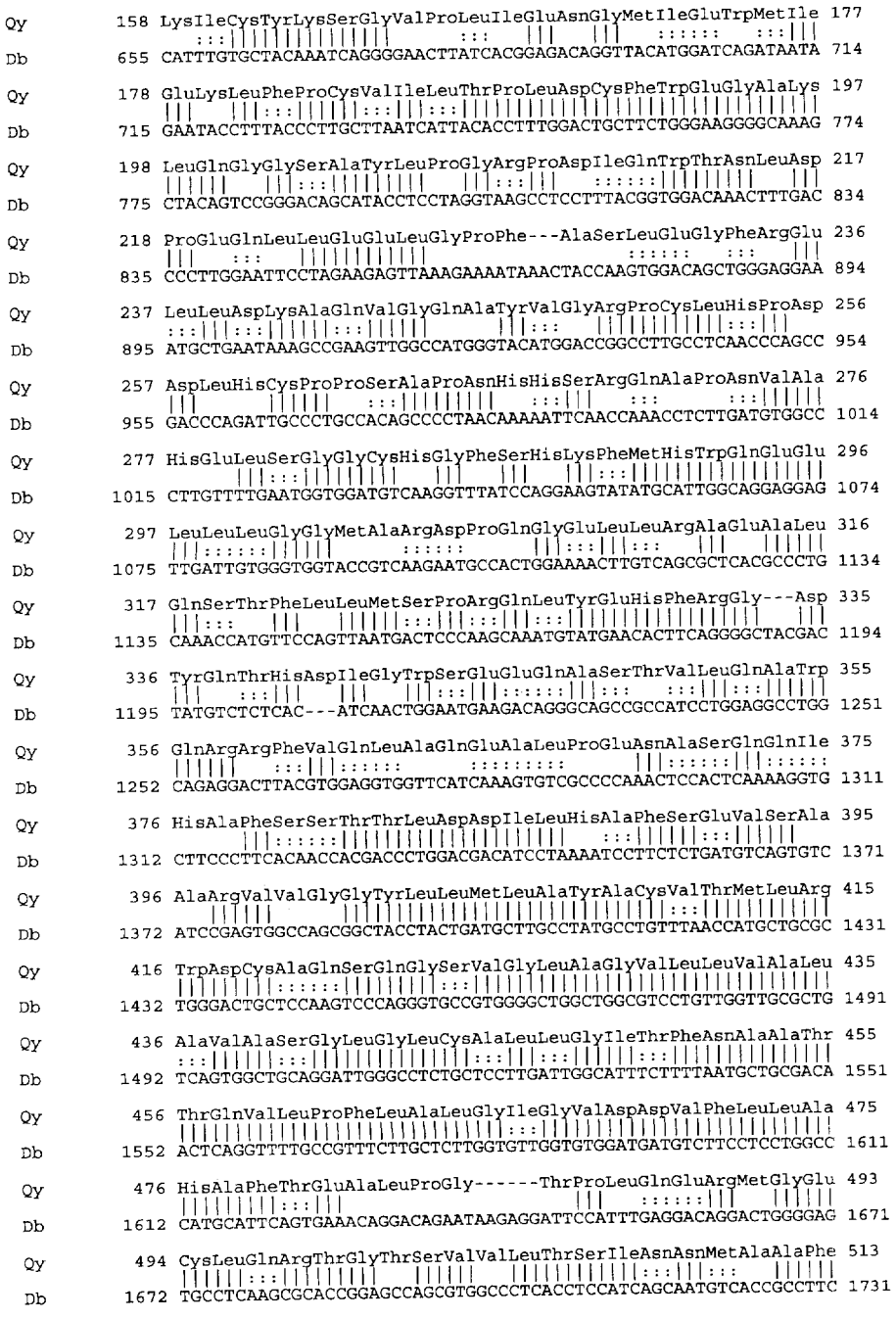
```
RESULT 10
US-09-754-032-3
; Sequence 3, Application US/09754032
; Publication No. US20030148388A1
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,032
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/540,406
;             FILING DATE: 06-OCT-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5187 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-032-3

Alignment Scores:
Pred. No.:                6.28e-303      Length:          5187
Score:                    3337.00        Matches:         677
Percent Similarity:       69.59%         Conservative:    204
Best Local Similarity:    53.48%         Mismatches:      306
Query Match:              53.20%         Indels:          80
DB:                       10             Gaps:            20

US-09-990-046-2 (1-1203) x US-09-754-032-3 (1-5187)

Qy          3 ArgSerProProLeuArgGluLeu------ProProSerTyrThrProProAlaArgThr 20

Db        178 CGCGCCGCGCCGGACCGGGACTATCTGCACCGGCCCAGCTACTGC---GACGCCGCCTTC 234

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeu---------LysAlaProLeuTrpLeuArg 37

Db        235 GCTCTGGAGCAGATTTCCAAGGGGAAGGCTACTGGCCGGAAAGCGCCGCTGTGGCTGAGA 294

Qy         38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57

Db        295 GCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTACATTCAAAAGAACTGCGGCAAG 354

Qy         58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77

Db        355 TTTTTGGTTGTGGGTCTCCTCATATTTGGGGCCTTCGCTGTGGGATTAAAGGCAGCTAAT 414

Qy         78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97

Db        415 CTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGTGGACGAGTGAGTCGAGAATTA 474

Qy         98 HisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117

Db        475 AATTATACCCGTCAGAAGATAGGAGAAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534

Qy        118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137

Db        535 ACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACAGAGGCTCTCCTGCAACACCTGGAC 594

Qy        138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157

Db        595 TCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATGTATAACAGGCAATGGAAGTTGGAA 654

Qy        158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177

Db        655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714

Qy        178 GluLysLeuProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197

Db        715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774

Qy        198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217

Db        775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834

Qy        218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236

Db        835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894

Qy        237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256

Db        895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954
```


Qy 257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
Db 955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014
Qy 277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296
Db 1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074
Qy 297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316
Db 1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134
Qy 317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
Db 1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194
Qy 336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db 1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251
Qy 356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
Db 1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311
Qy 376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
Db 1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371
Qy 396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
Db 1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431
Qy 416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
Db 1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491
Qy 436 AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr 455
Db 1492 TCAGTGGCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACA 1551
Qy 456 ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla 475
Db 1552 ACTCAGGTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCC 1611
Qy 476 HisAlaPheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGlu 493
Db 1612 CATGCATTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAG 1671
Qy 494 CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe 513
Db 1672 TGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTC 1731
Qy 514 LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
Db 1732 TTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 1791
Qy 534 ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp 553
Db 1792 GTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATTTTTCCTGCAATTCTCAGCATGGAT 1851
Qy 554 LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer 573
Db 1852 TTATACAGACGTGAGGACAGAAGATTGGATATTTTCTGCTGTTTCACAAGCCCCTGTGTC 1911
Qy 574 AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIl 593
Db 1912 AGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACAGAGCCTCACAGTAACACCCGGTAC 1971
Qy 593 eAla---------HisLeuThrAlaThrValGln---------- 601
Db 1972 AGCCCCCCACCCCCATACACCAGCCACAGCTTCGCCCACGAAACCCATATCACTATGCAG 2031
Qy 602 ----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
Db 2032 TCCACCGTTCAGCTCCGCACAGAGTATGACCCTCACACGCACGTGTACTACACCACCGCC 2091
Qy 620 nAlaHis--------------------LeuValProProProSerAspProLeuGlySe 633
Db 2092 GAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACCGTCACCCAG-GACAACCTCAGCTG 2150
Qy 633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThrAr 653
Db 2151 TCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCTGCTCTCCCAGTTCTCAGACTCC-- 2208
Qy 653 gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db 2209 ----AGCCTCCACTGCCTCGAGCCCCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA 2264
Qy 673 gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh 693
Db 2265 GAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGCCAAGGTTGTGGTAATCCTTCTTTT 2324
Qy 693 eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db 2325 CCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACCCGAGTGAGAGACGGGCTGGACCT 2384
Qy 713 uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db 2385 CACGGACATTGTTCCCCGGGAAACCAGAGAATATGACTTCATAGCTGCCCAGTTCAAGTA 2444
Qy 733 rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db 2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA---GACTACCCGAATATCCA 2501
Qy 753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
Db 2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561
Qy 773 oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGl 793
Db 2562 GAACAAGCAACTTCCCCAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
Qy 793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813
Db 2622 GGATGCATTTGACAGTGACTGGGAAACTGGGAGGATCATGCCAAACAATTATAAAAATGG 2681
Qy 813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
Db 2682 ATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGTGCAGACTGGCAGCCGAGACAAGCC 2741
Qy 833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853
Db 2742 CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGCAGATGGCATCATTAATCC 2801
Qy 853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
Db 2802 GAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGACCCTGTAGCTTACGCTGC 2861
Qy 873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893
Db 2862 CTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCATGACAAAGCCGACTACAT 2921
Qy 893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db 2922 GCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCCTTT 2981
Qy 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db 2982 CTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAAGTGAGAGT 3041
Qy 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db 3042 CATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTTCCT 3101
Qy 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972



```
RESULT 11
US-09-754-032-9
; Sequence 9, Application US/09754032
; Publication No. US20030148388A1
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,032
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/540,406
;             FILING DATE: 06-OCT-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5187 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-754-032-9

Alignment Scores:
Pred. No.:                6.28e-303     Length:          5187
Score:                    3337.00       Matches:         677
Percent Similarity:       69.59%        Conservative:    204
Best Local Similarity:    53.48%        Mismatches:      306
Query Match:              53.20%        Indels:          80
DB:                       10            Gaps:            20

US-09-990-046-2 (1-1203) x US-09-754-032-9 (1-5187)
```




Qy 158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
Db 655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714
Qy 178 GluLysLeuProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
Db 715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774
Qy 198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
Db 775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834
Qy 218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db 835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894
Qy 237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db 895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954
Qy 257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
Db 955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014
Qy 277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296
Db 1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074
Qy 297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316
Db 1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134
Qy 317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
Db 1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194
Qy 336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db 1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251
Qy 356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
Db 1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311
Qy 376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
Db 1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371
Qy 396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
Db 1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431
Qy 416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
Db 1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491
Qy 436 AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr 455
Db 1492 TCAGTGGCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACA 1551
Qy 456 ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla 475
Db 1552 ACTCAGGTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCC 1611
Qy 476 HisAlaPheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGlu 493
Db 1612 CATGCATTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAG 1671
Qy 494 CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe 513
Db 1672 TGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTC 1731
Qy 514 LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
Db 1732 TTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 1791
Qy 534 ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp 553
Db 1792 GTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATTTTCCTGCAATTCTCAGCATGGAT 1851
Qy 554 LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer 573
Db 1852 TTATACAGACGTGAGGACAGAAGATTGGATATTTTCTGCTGTTTCACAAGCCCCTGTGTC 1911
Qy 574 AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIl 593
Db 1912 AGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACAGAGCCTCACAGTAACACCCGGTAC 1971
Qy 593 eAla---------HisLeuThrAlaThrValGln---------- 601
Db 1972 AGCCCCCCACCCCCATACACCAGCCACAGCTTCGCCCACGAAACCCATATCACTATGCAG 2031
Qy 602 ----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
Db 2032 TCCACCGTTCAGCTCCGCACAGAGTATGACCCTCACACGCACGTGTACTACACCACCGCC 2091
Qy 620 nAlaHis----------LeuValProProProSerAspProLeuGlySe 633
Db 2092 GAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACCGTCACCCAG-GACAACCTCAGCTG 2150
Qy 633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThrAr 653
Db 2151 TCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCTGCTCTCCCAGTTCTCAGACTCC-- 2208
Qy 653 gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db 2209 ----AGCCTCCACTGCCTCGAGCCCCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA 2264
Qy 673 gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh 693
Db 2265 GAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGCCAAGGTTGTGGTAATCCTTCTTTT 2324
Qy 693 eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db 2325 CCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACCCGAGTGAGAGACGGGCTGGACCT 2384
Qy 713 uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db 2385 CACGGACATTGTTCCCCGGGAAACCAGAGAATATGACTTCATAGCTGCCCAGTTCAAGTA 2444
Qy 733 rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db 2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA---GACTACCCGAATATCCA 2501
Qy 753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
Db 2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561
Qy 773 oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGl 793
Db 2562 GAACAAGCAACTTCCCCAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
Qy 793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813
Db 2622 GGATGCATTTGACAGTGACTGGGAAACTGGGAGGATCATGCCAAACAATTATAAAAATGG 2681
Qy 813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
Db 2682 ATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGTGCAGACTGGCAGCCGAGACAAGCC 2741
Qy 833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853
Db 2742 CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGCAGATGGCATCATTAATCC 2801
Qy 853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873

```
Db       2802 GAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGACCCTGTAGCTTACGCTGC 2861

Qy        873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893

Db       2862 CTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCATGACAAAGCCGACTACAT 2921

Qy        893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912

Db       2922 GCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCCTTT 2981

Qy        912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932

Db       2982 CTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAAGTGAGAGT 3041

Qy        932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952

Db       3042 CATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTTCCT 3101

Qy        952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972

Db       3102 GTTCTGGGAGCAATACATCAGCCTGCGCCACTGGCTGCTGCTATCCATCAGCGTGGTGCT 3161

Qy        972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992

Db       3162 GGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCTGAACCCCTGGACGGCCGGGATCAT 3221

Qy        992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl 1012

Db       3222 TGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCCTCATTGGGAT 3281

Qy       1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032

Db       3282 CAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGCATCTGTTGGCATCGGAGTGGAGTT 3341

Qy       1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052

Db       3342 CACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCATTGGGGACAAGAACCACAGGGCTAT 3401

Qy       1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072

Db       3402 GCTCGCTCTGGAACACATGTTTGCTCCCGTTCTGGACGGTGCTGTGTCCACTCTGCTGGG 3461

Qy       1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092

Db       3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTCAGATACTTCTTTGCCGTCCT 3521

Qy       1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

Db       3522 GGCCATTCTCACCGTCTTGGGGGTTCTCAATGGACTGGTTCTGCTGCCTGTCCTCTTATC 3581

Qy       1112 rIleLeuGlyProProProGluValIle----------------GlnMetTyrLysGl 1126

Db       3582 CTTCTTTGGACCGTGTCCTGAGGTGTCTCCAGCCAATGGCCTAAACCGACTGCCCACTCC 3641

Qy       1126 uSerProGluIleLeuSerProPro--------------AlaProGlnGlyGlyGlyLe 1141

Db       3642 TTCGCCTGAG------CCGCCTCCAAGTGTCGTCCGGTTTGCCGTGCCTCCTGGTCACAC 3695

Qy       1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159

Db       3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755

Qy       1159 ------------------------------------------------------------ 1159

Db       3756 CAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGGTGCCGGAGGCCCTGCCCACCAAGT 3815

Qy       1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177

Db       3816 GATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCGGTCCACTGTGGTCCATCCGGACTC 3875

Qy       1177 aProAspGluProProTrpSerProAlaAla---------ThrSerSerGlyAsnLeuSe 1194

Db       3876 CAGACATCAGCCTCCCTTGACCCCTCGGCAACAGCCCCACCTGGACTCTGGCTCCTTGTC 3935

Qy       1194 rSerArgGlyProGly 1199

Db       3936 C---------CCTGGA 3942
```

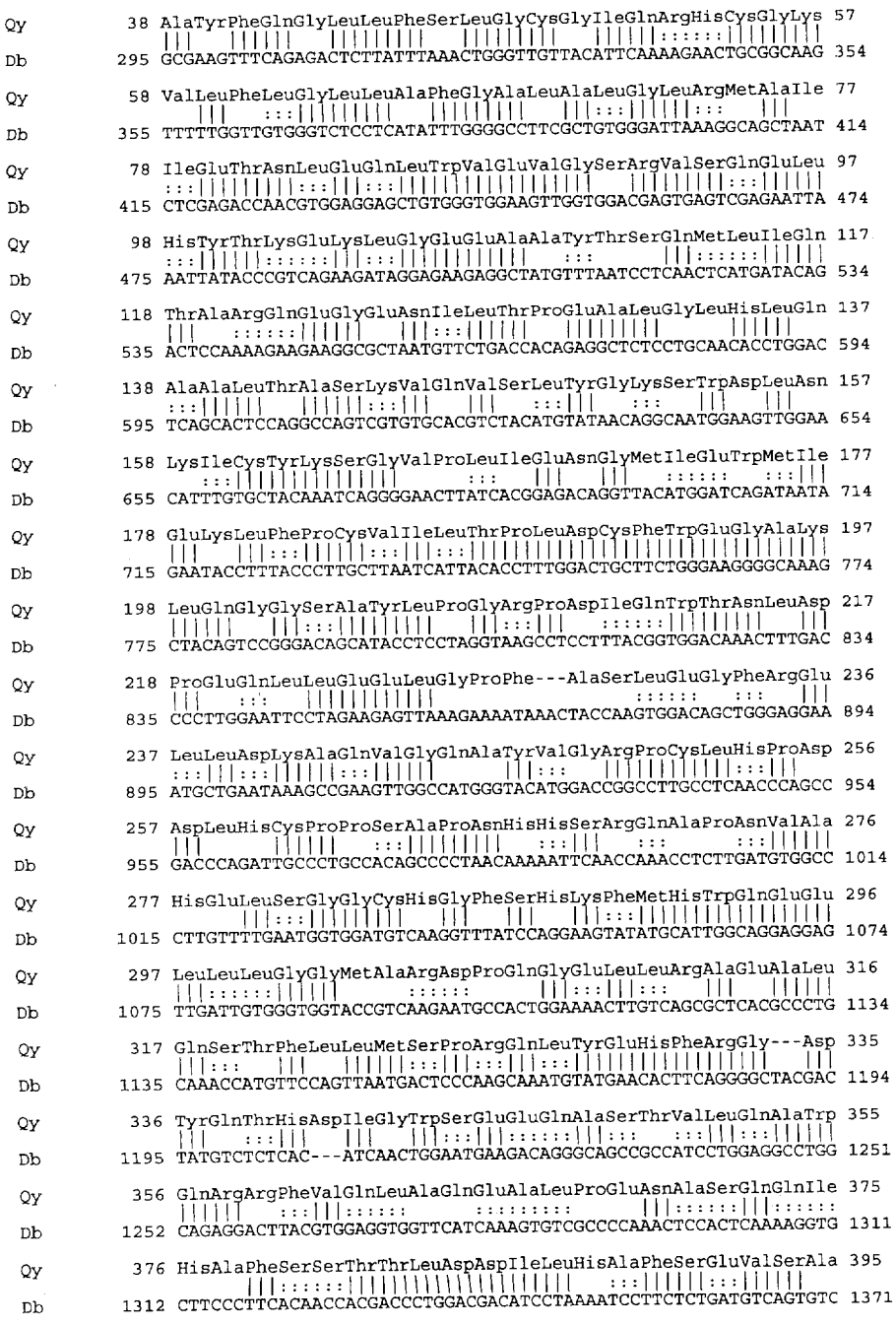
RESULT 12
US-10-421-446-3
; Sequence 3, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-421-446-3

Alignment Scores:

Pred. No.:	6.28e-303	Length:	5187
Score:	3337.00	Matches:	677
Percent Similarity:	69.59%	Conservative:	204
Best Local Similarity:	53.48%	Mismatches:	306
Query Match:	53.20%	Indels:	80
DB:	15	Gaps:	20

US-09-990-046-2 (1-1203) x US-10-421-446-3 (1-5187)

```
Qy          3 ArgSerProProLeuArgGluLeu------ProProSerTyrThrProProAlaArgThr 20

Db        178 CGCGCCGCGCCGGACCGGGACTATCTGCACCGGCCCAGCTACTGC---GACGCCGCCTTC 234

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeu---------LysAlaProLeuTrpLeuArg 37

Db        235 GCTCTGGAGCAGATTTCCAAGGGGAAGGCTACTGGCCGGAAAGCGCCGCTGTGGCTGAGA 294
```


Qy 38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db 295 GCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTACATTCAAAAGAACTGCGGCAAG 354
Qy 58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
Db 355 TTTTTGGTTGTGGGTCTCCTCATATTTGGGGCCTTCGCTGTGGGATTAAAGGCAGCTAAT 414
Qy 78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
Db 415 CTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGTGGACGAGTGAGTCGAGAATTA 474
Qy 98 HisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
Db 475 AATTATACCCGTCAGAAGATAGGAGAAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534
Qy 118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137
Db 535 ACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACAGAGGCTCTCCTGCAACACCTGGAC 594
Qy 138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
Db 595 TCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATGTATAACAGGCAATGGAAGTTGGAA 654
Qy 158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
Db 655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714
Qy 178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
Db 715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774
Qy 198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
Db 775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834
Qy 218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db 835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894
Qy 237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db 895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954
Qy 257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
Db 955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014
Qy 277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296
Db 1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074
Qy 297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316
Db 1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134
Qy 317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
Db 1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194
Qy 336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db 1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251
Qy 356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
Db 1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311
Qy 376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
Db 1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371
Qy 396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
Db 1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431
Qy 416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
Db 1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491
Qy 436 AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr 455
Db 1492 TCAGTGGCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACA 1551
Qy 456 ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla 475
Db 1552 ACTCAGGTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCC 1611
Qy 476 HisAlaPheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGlu 493
Db 1612 CATGCATTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAG 1671
Qy 494 CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe 513
Db 1672 TGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTC 1731
Qy 514 LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
Db 1732 TTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 1791
Qy 534 ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp 553
Db 1792 GTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATTTTTCCTGCAATTCTCAGCATGGAT 1851
Qy 554 LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer 573
Db 1852 TTATACAGACGTGAGGACAGAAGATTGGATATTTTCTGCTGTTTCACAAGCCCCTGTGTC 1911
Qy 574 AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIl 593
Db 1912 AGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACAGAGCCTCACAGTAACACCCGGTAC 1971
Qy 593 eAla---------HisLeuThrAlaThrValGln---------- 601
Db 1972 AGCCCCCCACCCCCATACACCAGCCACAGCTTCGCCCACGAAACCCATATCACTATGCAG 2031
Qy 602 ----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
Db 2032 TCCACCGTTCAGCTCCGCACAGAGTATGACCCTCACACGCACGTGTACTACACCACCGCC 2091
Qy 620 nAlaHis----------LeuValProProProSerAspProLeuGlySe 633
Db 2092 GAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACCGTCACCCAG-GACAACCTCAGCTG 2150
Qy 633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThrAr 653
Db 2151 TCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCTGCTCTCCCAGTTCTCAGACTCC-- 2208
Qy 653 gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db 2209 ----AGCCTCCACTGCCTCGAGCCCCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA 2264
Qy 673 gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh 693
Db 2265 GAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGCCAAGGTTGTGGTAATCCTTCTTTT 2324
Qy 693 eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db 2325 CCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACCCGAGTGAGAGACGGGCTGGACCT 2384
Qy 713 uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db 2385 CACGGACATTGTTCCCCGGGAAACCAGAGAATATGACTTCATAGCTGCCCAGTTCAAGTA 2444
Qy 733 rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753

```
Db       2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA---GACTACCCGAATATCCA 2501

Qy        753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773

Db       2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561

Qy        773 oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGl 793

Db       2562 GAACAAGCAACTTCCCCAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621

Qy        793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813

Db       2622 GGATGCATTTGACAGTGACTGGGAAACTGGGAGGATCATGCCAAACAATTATAAAAATGG 2681

Qy        813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833

Db       2682 ATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGTGCAGACTGGCAGCCGAGACAAGCC 2741

Qy        833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853

Db       2742 CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGCAGATGGCATCATTAATCC 2801

Qy        853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873

Db       2802 GAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGACCCTGTAGCTTACGCTGC 2861

Qy        873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893

Db       2862 CTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCATGACAAAGCCGACTACAT 2921

Qy        893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912

Db       2922 GCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCCTTT 2981

Qy        912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932

Db       2982 CTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAAGTGAGAGT 3041

Qy        932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952

Db       3042 CATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTTCCT 3101

Qy        952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972

Db       3102 GTTCTGGGAGCAATACATCAGCCTGCGCCACTGGCTGCTGCTATCCATCAGCGTGGTGCT 3161

Qy        972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992

Db       3162 GGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCTGAACCCCTGGACGGCCGGGATCAT 3221

Qy        992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl 1012

Db       3222 TGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCCTCATTGGGAT 3281

Qy       1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032

Db       3282 CAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGCATCTGTTGGCATCGGAGTGGAGTT 3341

Qy       1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052

Db       3342 CACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCATTGGGGACAAGAACCACAGGGCTAT 3401

Qy       1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072

Db       3402 GCTCGCTCTGGAACACATGTTTGCTCCCGTTCTGGACGGTGCTGTGTCCACTCTGCTGGG 3461

Qy       1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092

Db       3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTCAGATACTTCTTTGCCGTCCT 3521

Qy       1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

Db       3522 GGCCATTCTCACCGTCTTGGGGGTTCTCAATGGACTGGTTCTGCTGCCTGTCCTCTTATC 3581

Qy       1112 rIleLeuGlyProProProGluValIle----------------GlnMetTyrLysGl 1126

Db       3582 CTTCTTTGGACCGTGTCCTGAGGTGTCTCCAGCCAATGGCCTAAACCGACTGCCCACTCC 3641

Qy       1126 uSerProGluIleLeuSerProPro--------------AlaProGlnGlyGlyGlyLe 1141

Db       3642 TTCGCCTGAG------CCGCCTCCAAGTGTCGTCCGGTTTGCCGTGCCTCCTGGTCACAC 3695

Qy       1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159

Db       3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755

Qy       1159 ---------------------------------------------------------- 1159

Db       3756 CAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGGTGCCGGAGGCCCTGCCCACCAAGT 3815

Qy       1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177

Db       3816 GATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCGGTCCACTGTGGTCCATCCGGACTC 3875

Qy       1177 aProAspGluProProTrpSerProAlaAla---------ThrSerSerGlyAsnLeuSe 1194

Db       3876 CAGACATCAGCCTCCCTTGACCCCTCGGCAACAGCCCCACCTGGACTCTGGCTCCTTGTC 3935

Qy       1194 rSerArgGlyProGly 1199

Db       3936 C---------CCTGGA 3942
```

RESULT 13
US-10-421-446-9
; Sequence 9, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs

```
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-421-446-9

Alignment Scores:
Pred. No.:                6.28e-303      Length:          5187
Score:                    3337.00        Matches:         677
Percent Similarity:       69.59%         Conservative:    204
Best Local Similarity:    53.48%         Mismatches:      306
Query Match:              53.20%         Indels:          80
DB:                       15             Gaps:            20

US-09-990-046-2 (1-1203) x US-10-421-446-9 (1-5187)

Qy          3 ArgSerProProLeuArgGluLeu------ProProSerTyrThrProProAlaArgThr 20
              |||:::   |||   |||:::           |||||||||          |||
Db        178 CGCGCCGCGCCGGACCGGGACTATCTGCACCGGCCCAGCTACTGC---GACGCCGCCTTC 234

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeu---------LysAlaProLeuTrpLeuArg 37
              |||      ||||||      |||                ||||||||||||||||||||
Db        235 GCTCTGGAGCAGATTTCCAAGGGGAAGGCTACTGGCCGGAAAGCGCCGCTGTGGCTGAGA 294

Qy         38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
              |||   ||||||   |||||||||   |||||||||   ||||||::::::|||||||||
Db        295 GCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTACATTCAAAAGAACTGCGGCAAG 354

Qy         58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
                 |||   :::||||||||||   |||||||||   |||:::||||||:::   |||
Db        355 TTTTTGGTTGTGGGTCTCCTCATATTTGGGGCCTTCGCTGTGGGATTAAAGGCAGCTAAT 414

Qy         78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
              :::||||||||||:::|||:::|||||||||||||||||||   ||||||||:::||||||
Db        415 CTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGTGGACGAGTGAGTCGAGAATTA 474

Qy         98 HisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
              :::||||||:::::|||:::||||||||||||   :::      |||:::::||||||
Db        475 AATTATACCCGTCAGAAGATAGGAGAAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534

Qy        118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137
              |||   ::::::||||||   |||:::||||||   |||||||||      ||||||
Db        535 ACTCCAAAAGAAGAAGGCGCTAATGTTCTGACCACAGAGGCTCTCCTGCAACACCTGGAC 594

Qy        138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
              :::||||||   ||||||:::|||   |||   :::|||   :::   |||   |||
Db        595 TCAGCACTCCAGGCCAGTCGTGTGCACGTCTACATGTATAACAGGCAATGGAAGTTGGAA 654

Qy        158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
              :::|||||||||||||||      :::   |||   |||   ::::::   :::|||
Db        655 CATTTGTGCTACAAATCAGGGGAACTTATCACGGAGACAGGTTACATGGATCAGATAATA 714

Qy        178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
              |||   |||:::||||||:::|||:::|||||||||||||||||||||||||||||||
Db        715 GAATACCTTTACCCTTGCTTAATCATTACACCTTTGGACTGCTTCTGGGAAGGGGCAAAG 774

Qy        198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
              ||||||   |||:::||||||||||   |||:::|||   ::::::||||||||   |||
Db        775 CTACAGTCCGGGACAGCATACCTCCTAGGTAAGCCTCCTTTACGGTGGACAAACTTTGAC 834

Qy        218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
              |||   :::   ||||||||||||                ::::::   :::   |||
Db        835 CCCTTGGAATTCCTAGAAGAGTTAAAGAAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894

Qy        237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
              :::|||:::|||||||:::||||||      |||:::   ||||||||||||:::|||
Db        895 ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCCTTGCCTCAACCCAGCC 954

Qy        257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
              |||      ||||||   :::||||||||   :::|||   :::      :::|||||||
Db        955 GACCCAGATTGCCCTGCCACAGCCCCTAACAAAAATTCAACCAAACCTCTTGATGTGGCC 1014

Qy        277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu 296
              |||:::||||||||||   |||   |||   |||:::||||||||||||||||||||
Db       1015 CTTGTTTTGAATGGTGGATGTCAAGGTTTATCCAGGAAGTATATGCATTGGCAGGAGGAG 1074

Qy        297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu 316
              |||::::::||||||      ::::::      |||::|||:::   |||   ||||||
Db       1075 TTGATTGTGGGTGGTACCGTCAAGAATGCCACTGGAAAACTTGTCAGCGCTCACGCCCTG 1134

Qy        317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
              |||:::   |||   ||||||:::|||:::|||:::|||||||||||||||||   |||
Db       1135 CAAACCATGTTCCAGTTAATGACTCCCAAGCAAATGTATGAACACTTCAGGGGCTACGAC 1194

Qy        336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
              |||   :::|||   |||   |||:::|||::::::|||:::   :::||||:::||||||
Db       1195 TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCCGCCATCCTGGAGGCCTGG 1251

Qy        356 GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle 375
              ||||||   :::|||::::::      :::::::::      |||::::::|||::::::
Db       1252 CAGAGGACTTACGTGGAGGTGGTTCATCAAAGTGTCGCCCCAAACTCCACTCAAAAGGTG 1311

Qy        376 HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla 395
                 |||::::::||||||||||||||||||||||||||||   :::|||||||:::||||||
Db       1312 CTTCCCTTCACAACCACGACCCTGGACGACATCCTAAAATCCTTCTCTGATGTCAGTGTC 1371

Qy        396 AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg 415
              ||||||   ||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1372 ATCCGAGTGGCCAGCGGCTACCTACTGATGCTTGCCTATGCCTGTTTAACCATGCTGCGC 1431

Qy        416 TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu 435
              |||||||||:::::||||||||:::||||||||||||||||||||||||||||||||||
Db       1432 TGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCTGGCGTCCTGTTGGTTGCGCTG 1491

Qy        436 AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr 455
              :::||||||:::|||||||||||||:::|||:::||||||:::|||||||||||||||||
Db       1492 TCAGTGGCTGCAGGATTGGGCCTCTGCTCCTTGATTGGCATTTCTTTTAATGCTGCGACA 1551

Qy        456 ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla 475
              ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db       1552 ACTCAGGTTTTGCCGTTTCTTGCTCTTGGTGTTGGTGTGGATGATGTCTTCCTCCTGGCC 1611

Qy        476 HisAlaPheThrGluAlaLeuProGly------ThrProLeuGlnGluArgMetGlyGlu 493
              |||||||||:::|||                  |||   ::::::|||   ||||||
Db       1612 CATGCATTCAGTGAAACAGGACAGAATAAGAGGATTCCATTTGAGGACAGGACTGGGGAG 1671

Qy        494 CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe 513
              ||||||:::|||||||||   ||||||   ||||||||||||:::|||:::   ||||||
Db       1672 TGCCTCAAGCGCACCGGAGCCAGCGTGGCCCTCACCTCCATCAGCAATGTCACCGCCTTC 1731

Qy        514 LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||:::
Db       1732 TTCATGGCCGCATTGATCCCTATCCCTGCCCTGCGAGCGTTCTCCCTCCAGGCTGCTGTG 1791

Qy        534 ValValGlyCysThrPheValAlaValMetLeuValProProAlaIleLeuSerLeuAsp 553
              ||||||      |||      |||:::|||:::|||||||||||||||||:::|||
Db       1792 GTGGTGGTATTCAATTTTGCTATGGTTCTGCTCATTTTTCCTGCAATTCTCAGCATGGAT 1851

Qy        554 LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer 573
              |||   ||||||      :::||||||||:::   ||||||||||:::||||||||||
Db       1852 TTATACAGACGTGAGGACAGAAGATTGGATATTTTCTGCTGTTTCACAAGCCCCTGTGTC 1911

Qy        574 AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIl 593
              ::::::||||||||:::   ||||||      :::   ||||||      |||
Db       1912 AGCAGGGTGATTCAAGTTGAGCCACAGGCCTACACAGAGCCTCACAGTAACACCCGGTAC 1971

Qy        593 eAla---------HisLeuThrAlaThrValGln------------------------- 601
               |||      |||      ||||||
Db       1972 AGCCCCCCACCCCCATACACCAGCCACAGCTTCGCCCACGAAACCCATATCACTATGCAG 2031

Qy        602 ----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
                  |||:::      ::::::   :::                        ||||||
Db       2032 TCCACCGTTCAGCTCCGCACAGAGTATGACCCTCACACGCACGTGTACTACACCACCGCC 2091

Qy        620 nAlaHis--------------------LeuValProProProSerAspProLeuGlySe 633
```

```
Db       2092 GAGCCACGCTCTGAGATCTCTGTACAGCCTGTTACCGTCACCCAG-GACAACCTCAGCTG 2150
Qy        633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluGluThrAr 653
Db       2151 TCAGAGTCCCGAGAGCACCAGCTCTACCAGGGACCTGCTCTCCCAGTTCTCAGACTCC-- 2208
Qy        653 gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db       2209 ----AGCCTCCACTGCCTCGAGCCCCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA 2264
Qy        673 gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh 693
Db       2265 GAAGCACTATGCTCCTTTCCTCCTGAAACCCAAAGCCAAGGTTGTGGTAATCCTTCTTTT 2324
Qy        693 eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db       2325 CCTGGGCTTGCTGGGGGTCAGCCTTTATGGGACCACCCGAGTGAGAGACGGGCTGGACCT 2384
Qy        713 uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db       2385 CACGGACATTGTTCCCCGGGAAACCAGAGAATATGACTTCATAGCTGCCCAGTTCAAGTA 2444
Qy        733 rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db       2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA---GACTACCCGAATATCCA 2501
Qy        753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
Db       2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561
Qy        773 oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGl 793
Db       2562 GAACAAGCAACTTCCCCAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
Qy        793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813
Db       2622 GGATGCATTTGACAGTGACTGGGAAACTGGGAGGATCATGCCAAACAATTATAAAAATGG 2681
Qy        813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
Db       2682 ATCAGATGACGGGGTCCTCGCTTACAAACTCCTGGTGCAGACTGGCAGCCGAGACAAGCC 2741
Qy        833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853
Db       2742 CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGCAGATGGCATCATTAATCC 2801
Qy        853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
Db       2802 GAGCGCTTTCTACATCTACCTGACCGCTTGGGTCAGCAACGACCCTGTAGCTTACGCTGC 2861
Qy        873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893
Db       2862 CTCCCAGGCCAACATCCGGCCTCACCGGCCGGAGTGGGTCCATGACAAAGCCGACTACAT 2921
Qy        893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db       2922 GCCAGAGACCAGGCTGAGAATCCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCCTTT 2981
Qy        912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db       2982 CTACCTCAACGGCCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAAGTGAGAGT 3041
Qy        932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db       3042 CATCTGTAACAACTATACGAGCCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTTCCT 3101
Qy        952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db       3102 GTTCTGGGAGCAATACATCAGCCTGCGCCACTGGCTGCTGCTATCCATCAGCGTGGTGCT 3161
Qy        972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
Db       3162 GGCCTGCACGTTTCTAGTGTGCGCAGTCTTCCTCCTGAACCCCTGGACGGCCGGGATCAT 3221
Qy        992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl 1012
Db       3222 TGTCATGGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCCTCATTGGGAT 3281
Qy       1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032
Db       3282 CAAGCTGAGTGCTGTGCCTGTGGTCATCCTGATTGCATCTGTTGGCATCGGAGTGGAGTT 3341
Qy       1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
Db       3342 CACCGTCCACGTGGCTTTGGCCTTTCTGACAGCCATTGGGGACAAGAACCACAGGGCTAT 3401
Qy       1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072
Db       3402 GCTCGCTCTGGAACACATGTTTGCTCCCGTTCTGGACGGTGCTGTGTCCACTCTGCTGGG 3461
Qy       1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092
Db       3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTCAGATACTTCTTTGCCGTCCT 3521
Qy       1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112
Db       3522 GGCCATTCTCACCGTCTTGGGGGTTCTCAATGGACTGGTTCTGCTGCCTGTCCTCTTATC 3581
Qy       1112 rIleLeuGlyProProProGluValIle----------------GlnMetTyrLysGl 1126
Db       3582 CTTCTTTGGACCGTGTCCTGAGGTGTCTCCAGCCAATGGCCTAAACCGACTGCCCACTCC 3641
Qy       1126 uSerProGluIleLeuSerProPro---------------AlaProGlnGlyGlyGlyLe 1141
Db       3642 TTCGCCTGAG------CCGCCTCCAAGTGTCGTCCGGTTTGCCGTGCCTCCTGGTCACAC 3695
Qy       1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db       3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755
Qy       1159 ------------------------------------------------------------ 1159
Db       3756 CAGTGAGGAGCTCAGGCAATACGAAGCACAGCAGGGTGCCGGAGGCCCTGCCCACCAAGT 3815
Qy       1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177
Db       3816 GATTGTGGAAGCCACAGAAAACCCTGTCTTTGCCCGGTCCACTGTGGTCCATCCGGACTC 3875
Qy       1177 aProAspGluProProTrpSerProAlaAla---------ThrSerSerGlyAsnLeuSe 1194
Db       3876 CAGACATCAGCCTCCCTTGACCCCTCGGCAACAGCCCCACCTGGACTCTGGCTCCTTGTC 3935
Qy       1194 rSerArgGlyProGly 1199
Db       3936 C---------CCTGGA 3942
```

```
RESULT 14
US-10-302-279-1
; Sequence 1, Application US/10302279
; Publication No. US20030171566A1
;   GENERAL INFORMATION:
;        APPLICANT: Dean, Michael Carlton
;                   Hahn, Heidi Eve
;                   Wicking, Carol
;                   Christiansen, Jeffrey
;                   Zaphiropoulos, Peter G.
;                   Gailani, Mae R.
;                   Shanley, Susan Mary
;                   Chidambaram, Abirami
;                   Vorechovsky, Igor
;                   Holmberg-Lindstrom, Erika
;        TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
;        NUMBER OF SEQUENCES: 84
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
```

```
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;         COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/302,279
;            FILING DATE: 22-No. US20030171566A1-2002
;            CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/857,636
;            FILING DATE: 16-MAY-1997
;            APPLICATION NUMBER: US 60/017,906
;            FILING DATE: 17-MAY-1996
;            APPLICATION NUMBER: AU PO0011
;            FILING DATE: 21-MAY-1996
;            APPLICATION NUMBER: AU PO0363
;            FILING DATE: 07-JUN-1996
;            APPLICATION NUMBER: US 60/019,765
;            FILING DATE: 14-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Laurence J.
;            REGISTRATION NUMBER: 35, 551
;            REFERENCE/DOCKET NUMBER: 015280-278200US
;         TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;      INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;            LENGTH: 6568 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..6568
;            OTHER INFORMATION:  /note= "human nevoid basal cell
;            carcinoma syndrome (NBCCS)
;            (PATCHED (PTC)) cDNA"
;         FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  442..4332
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-302-279-1

Alignment Scores:
Pred. No.:                1.1e-302        Length:          6568
Score:                    3336.00         Matches:         664
Percent Similarity:       65.63%          Conservative:    205
Best Local Similarity:    50.15%          Mismatches:      273
Query Match:              53.19%          Indels:          182
DB:                       15              Gaps:            17

US-09-990-046-2 (1-1203) x US-10-302-279-1 (1-6568)

Qy         31 LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGly 50
Db        208 AAAGCGCCGCTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTAC 267

Qy         51 IleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAla 70
Db        268 ATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCCTTCGCG 327

Qy         71 LeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGluValGly 90
Db        328 GTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGA 387

Qy         91 SerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyr 110
Db        388 GGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCTATGTTT 447

Qy        111 ThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrProGlu 130
Db        448 AATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACCACAGAA 507

Qy        131 AlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeuTyr 150
Db        508 GCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATACATGTAC 567

Qy        151 GlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIleGluAsn 170
Db        568 AACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACAGAAACA 627

Qy        171 GlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrProLeuAsp 190
Db        628 GGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCTTTGGAC 687

Qy        191 CysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgProAsp 210
Db        688 TGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAACCTCCT 747

Qy        211 IleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe---Ala 229
Db        748 TTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATAAACTAT 807

Qy        230 SerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGly 249
Db        808 CAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTACATGGAC 867

Qy        250 ArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHisHisSer 269
Db        868 CGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAAAATTCA 927

Qy        270 ArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLys 289
Db        928 ACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCCAGAAAG 987

Qy        290 PheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlu 309
Db        988 TATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACTGGAAAA 1047

Qy        310 LeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyr 329
Db       1048 CTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAAATGTAC 1107

Qy        330 GluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGluGlnAla 348
Db       1108 GAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGACAAAGCG 1164

Qy        349 SerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuPro 368
Db       1165 GCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGTGTCGCA 1224

Qy        369 GluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHis 388
Db       1225 CAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATCCTGAAA 1284

Qy        389 AlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyr 408
Db       1285 TCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTCGCCTAT 1344

Qy        409 AlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeuAla 428
Db       1345 GCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCT 1404

Qy        429 GlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGly 448
Db       1405 GGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTGATCGGA 1464

Qy        449 IleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGlyVal 468
```

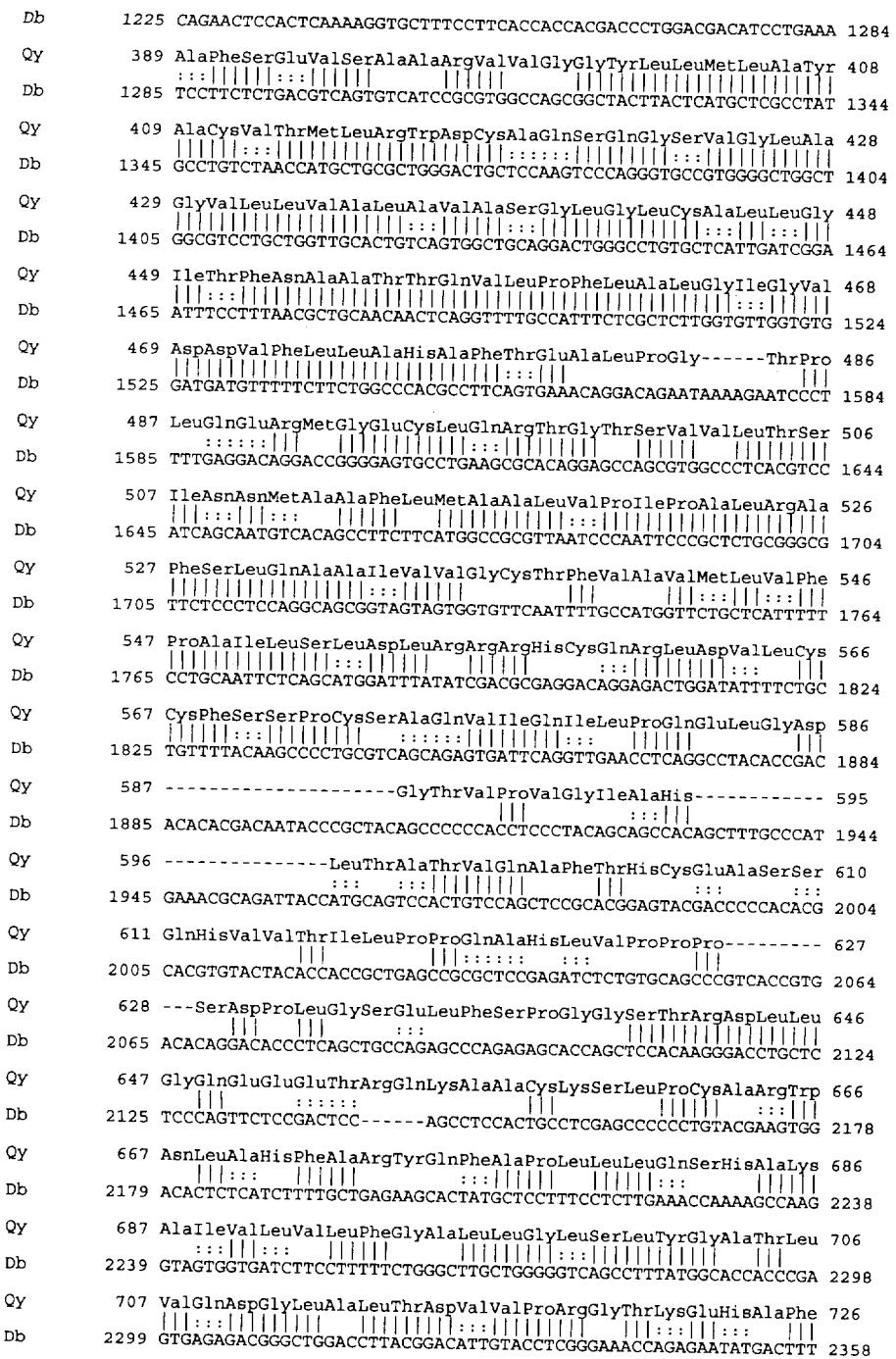
```
Qy    1121 -----------------------IleGlnMetTyr----------------------- 1124
                                  ::::::  |||
Db    3676 ACAGTGTCAGGCCTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGC 3735

Qy    1124 ------------------------------------------------------------ 1124

Db    3736 CCTGCCCACCAAGTGATCGTGGAAGCCACAGAAAACCCCGTCTTCGCCCACTCCACTGTG 3795

Qy    1125 ---------------------------------------LysGluSerProGluIleLeu 1131
                                                  |||:::   |||   :::
Db    3796 GTCCATCCCGAATCCAGGCATCACCCACCCTCGAACCCGAAACAGCAGCCCCACCTGGAC 3855

Qy    1132 Ser---------ProProAlaProGlnGly--------------------------Gly 1139
           |||         ||||||    ||||||
Db    3856 TCAGGGTCCCTGCCTCCCGGACGGCAAGGCCAGCAGCCCCGCAGGGACCCCCCAGAAAA 3915

Qy    1140 GlyLeu------------------------------------------------------ 1141
           ||||||
Db    3916 GGCTTGTGGCCACCCCTCTACAGACCGCGCAGAGACGCTTTTGAAATTTCTACTGAAGGG 3975

Qy    1142 -----------------------ArgTrpGly-------------------------- 1144
                                  |||||||||
Db    3976 CATTCTGGCCCTAGCAATAGGGCCCGCTGGGGCCCTCGCGGGGCCCGTTCTCACAACCCT 4035

Qy    1145 --------------------AlaSerSerSerLeuProGlnSerPheAlaArgValThr 1157
                                          ||||||:::|||           :::|||
Db    4036 CGGAACCCAACGTCCACTGCCATGGGCAGCTCCGTGCCCGGCTACTGCCAGCCCATCACC 4095

Qy    1158 Thr---------------SerMetThrValAlaIleHisProProProLeuProGlyAla 1172
           |||               |||:::|||||||||:::||||||||||||:::||||||
Db    4096 ACTGTGACGGCTTCTGCCTCCGTGACTGTCGCCGTGCACCCGCCGCCTGTCCCTGGGCCT 4155

Qy    1173 TyrIleHisPro 1176
              :::|||
Db    4156 GGGCGGAACCCC 4167
```

RESULT 15
US-09-964-824A-266
; Sequence 266, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 266
; LENGTH: 6568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6568)
; OTHER INFORMATION: n=a,t,g or c
US-09-964-824A-266

```
Alignment Scores:
Pred. No.:              4.99e-302     Length:         6568
Score:                  3329.00       Matches:        663
Percent Similarity:     65.56%        Conservative:   205
Best Local Similarity:  50.08%        Mismatches:     274
Query Match:            53.08%        Indels:         182
DB:                     9             Gaps:           17
```

US-09-990-046-2 (1-1203) x US-09-964-824A-266 (1-6568)

```
Qy      31 LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGly 50
           ||||||||||||||||||||||||     ||||||   |||||||||   |||||||||
Db     208 AAAGCGCCGCTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGTTGTTAC 267

Qy      51 IleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAla 70
           ||||||::::::|||||||||   |||    :::|||||||||   ||||||||   |||
Db     268 ATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCCTTCGCG 327

Qy      71 LeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGluValGly 90
           :::||||||:::   |||   :::|||||||||:::|||:::||||||||||||||||||
Db     328 GTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAAGTTGGA 387

Qy      91 SerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAlaAlaTyr 110
              ||||||||:::||||||:::||||||::::::|||:::||||||||||||   :::
Db     388 GGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCTATGTTT 447

Qy     111 ThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrProGlu 130
              |||::::::|||||||||   ::::::||||||   |||:::||||||   |||
Db     448 AATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACCACAGAA 507

Qy     131 AlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeuTyr 150
           ||||||         ||||||   :::||||||   ||||||:::|||   |||   :::|||
Db     508 GCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATACATGTAC 567

Qy     151 GlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIleGluAsn 170
            :::   |||   |||      :::|||||||||||||||||||   :::   |||
Db     568 AACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACAGAAACA 627

Qy     171 GlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrProLeuAsp 190
           |||   ::::::   :::||||||   |||:::||||||:::|||:::||||||||||||
Db     628 GGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCTTTGGAC 687

Qy     191 CysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgProAsp 210
           |||||||||||||||||||||||||   |||:::|||||||||   ||||||:::|||
Db     688 TGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAACCTCCT 747

Qy     211 IleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe---Ala 229
           ::::::||||||||   ||||||   :::   ||||||||||||
Db     748 TTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATAAACTAT 807

Qy     230 SerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGly 249
           ::::::   :::   |||:::|||:::||||||:::||||||      |||:::
Db     808 CAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTACATGGAC 867

Qy     250 ArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHisHisSer 269
           ||||||||||||:::|||   |||      ||||||   :::||||||||   :::|||
Db     868 CGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAAAATTCA 927

Qy     270 ArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLys 289
              :::      ::::::|||      |||:::|||||||||||||||   |||   |||
Db     928 ACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCCAGAAAG 987

Qy     290 PheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlu 309
           :::||||||||||||||||||||||||:::::::|||      ::::::      |||:::
Db     988 TATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACTGGAAAA 1047

Qy     310 LeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyr 329
           |||:::   |||   |||||||||:::   |||   ||||||:::|||:::|||:::|||
Db    1048 CTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAAATGTAC 1107

Qy     330 GluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGluGlnAla 348
           |||||||||:::|||   :::|||   :::|||   |||   |||:::|||::::::|||
Db    1108 GAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGACAAAGCG 1164

Qy     349 SerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuPro 368
           :::   :::|||:::||||||||||||   :::|||::::::      :::::::::
Db    1165 GCAGCCATCCTGGAGGCCTGGCAGAGGACATATGGAGGTGGTTCATCAGAGTGTCGCA 1224

Qy     369 GluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHis 388
           :::|||::::::|||::::::   :::|||::::::||||||||||||||||||
```


Db 1225 CAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATCCTGAAA 1284
Qy 389 AlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyr 408
Db 1285 TCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTCGCCTAT 1344
Qy 409 AlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeuAla 428
Db 1345 GCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGGCTGGCT 1404
Qy 429 GlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGly 448
Db 1405 GGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTGATCGGA 1464
Qy 449 IleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGlyVal 468
Db 1465 ATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTTGGTGTG 1524
Qy 469 AspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ThrPro 486
Db 1525 GATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGAATCCCT 1584
Qy 487 LeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeuThrSer 506
Db 1585 TTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTCACGTCC 1644
Qy 507 IleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArgAla 526
Db 1645 ATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTGCGGGCG 1704
Qy 527 PheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuValPhe 546
Db 1705 TTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTCATTTTT 1764
Qy 547 ProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspValLeuCys 566
Db 1765 CCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATTTTCTGC 1824
Qy 567 CysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGlyAsp 586
Db 1825 TGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTACACCGAC 1884
Qy 587 ----------GlyThrValProValGlyIleAlaHis---------- 595
Db 1885 ACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTTGCCCAT 1944
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSer 610
Db 1945 GAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCCCACACG 2004
Qy 611 GlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--------- 627
Db 2005 CACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTCACCGTG 2064
Qy 628 ---SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAspLeuLeu 646
Db 2065 ACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGACCTGCTC 2124
Qy 647 GlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrp 666
Db 2125 TCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACGAAGTGG 2178
Qy 667 AsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLys 686
Db 2179 ACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAAGCCAAG 2238
Qy 687 AlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeu 706
Db 2239 GTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACCACCCGA 2298
Qy 707 ValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAlaPhe 726
Db 2299 GTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATATGACTTT 2358
Qy 727 LeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGly 746
Db 2359 ATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA 2418
Qy 747 PheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeu 766
Db 2419 ---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGTAACGTG 2475
Qy 767 LysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArg 786
Db 2476 AAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTACTTCAGA 2535
Qy 787 AsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThr 806
Db 2536 GACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAAATCATG 2595
Qy 807 ArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGln 826
Db 2596 CCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTGGTGCAA 2655
Qy 827 ThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAsp 846
Db 2656 ACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTGGTGGAT 2715
Qy 847 ArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSerSer 866
Db 2716 GCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTCAGCAAC 2775
Qy 867 AspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeu 886
Db 2776 GACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAATGGGTC 2835
Qy 887 HisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeu 905
Db 2836 CACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAGCCCATC 2895
Qy 906 GluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGlu 925
Db 2896 GAGTATGCCCAGTTCCCTTTCTACCTCAACGGCTTGCGGGACACCTCAGACTTTGTGGAG 2955
Qy 926 AlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyr 945
Db 2956 GCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCCAGTTAC 3015
Qy 946 ProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeu 965
Db 3016 CCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGGCTGCTG 3075
Qy 966 LeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsn 985
Db 3076 CTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTGAAC 3135
Qy 986 ProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGly 1005
Db 3136 CCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCGGC 3195
Qy 1006 IleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSer 1025
Db 3196 ATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATCGCTTCT 3255
Qy 1026 ValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGly 1045
Db 3256 GTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCCATCAGC 3315
Qy 1046 SerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGly 1065
Db 3316 GACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTGGATGGC 3375
Qy 1066 AlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal 1085
Db 3376 GCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGACTTCGACTTCATTGTC 3435

```
Qy       1086 ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuVal 1105
             ||||||||||||||||   |||   :::||||||:::||||||:::|||:::||||||||||
Db       3436 AGGTATTTCTTTGCTGTGCTGGCAATCCTCACCATCCTCGGCGTTCTCAATGGGCTGGTT 3495

Qy       1106 LeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal--------------- 1120
             ||||||||||||||||   |||       ||||||   |||||||||
Db       3496 TTGCTTCCCGTGCTTTGGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCCAACGGC 3555

Qy       1120 ------------------------------------------------------------ 1120

Db       3556 TTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCGTGGTCCGCTTCGCCATG 3615

Qy       1120 ------------------------------------------------------------ 1120

Db       3616 CCGCCCGGCCACACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACG 3675

Qy       1121 ------------------------IleGlnMetTyr------------------------ 1124
                                      ::::::   |||
Db       3676 ACAGTGTCAGGCCTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGC 3735

Qy       1124 ------------------------------------------------------------ 1124

Db       3736 CCTGCCCACCAAGTGATCGTGGAAGCCACAGAAAACCCCGTCTTCGCCCACTCCACTGTG 3795

Qy       1125 ---------------------------------------LysGluSerProGluIleLeu 1131
                                                     |||:::   |||   :::
Db       3796 GTCCATCCCGAATCCAGGCATCACCCACCCTCGAACCCGAAACAGCAGCCCCACCTGGAC 3855

Qy       1132 Ser---------ProProAlaProGlnGly--------------------------Gly 1139
             |||          ||||||      ||||||
Db       3856 TCAGGGTCCCTGCCTCCCGGACGGCAAGGCCAGCAGCCCCGCAGGGACCCCCCCAGAAAA 3915

Qy       1140 GlyLeu------------------------------------------------------ 1141
             ||||||
Db       3916 GGCTTGTGGCCACCCCTCTACAGACCGCGCAGAGACGCTTTTGAAATTTCTACTGAAGGG 3975

Qy       1142 ------------------------ArgTrpGly-------------------------- 1144
                                      |||||||||
Db       3976 CATTCTGGCCCTAGCAATAGGGCCCGCTGGGGCCCTCGCGGGGCCCGTTCTCACAACCCT 4035

Qy       1145 --------------------AlaSerSerSerLeuProGlnSerPheAlaArgValThr 1157
                                   ||||||:::|||                :::|||
Db       4036 CGGAACCCAACGTCCACTGCCATGGGCAGCTCCGTGCCCGGCTACTGCCAGCCCATCACC 4095

Qy       1158 Thr---------------SerMetThrValAlaIleHisProProProLeuProGlyAla 1172
             |||               |||:::||||||||||:::||||||||||||:::||||||
Db       4096 ACTGTGACGGCTTCTGCCTCCGTGACTGTCGCCGTGCACCCGCCGCCTGTCCCTGGGCCT 4155

Qy       1173 TyrIleHisPro 1176
                 :::|||
Db       4156 GGGCGGAACCCC 4167
```

Search completed: November 22, 2004, 14:19:04
Job time : 1122 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:15 ; Search time 842 Seconds
(without alignments)
7500.064 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09990046/runat_21112004_130919_18522/app_query.fasta_1.1351
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990046_@CGN_1_1_478_@runat_21112004_130919_18522 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	4030	2	AAZ31717	Aaz31717 Human pat
2	6272	100.0	4030	6	AAD31576	Aad31576 Human pat
3	6272	100.0	4030	8	ABX15919	Abx15919 Human cDN
4	6248	99.6	4391	2	AAX89478	Aax89478 Human ptc
5	5911	94.2	3453	3	AAA09081	Aaa09081 Human pat
6	4682.5	74.7	12886	3	AAA09084	Aaa09084 Human pat
7	3955	63.1	4004	2	AAZ31728	Aaz31728 Human pat
8	3955	63.1	4004	6	AAD31580	Aad31580 Human pat
9	3955	63.1	4004	8	ABX15923	Abx15923 Human par
10	3387	54.0	2082	2	AAZ31729	Aaz31729 Human pat
11	3387	54.0	2082	6	AAD31581	Aad31581 Human pat
12	3387	54.0	2082	8	ABX15924	Abx15924 Human par
13	3349	53.4	5288	2	AAT14220	Aat14220 Human pat
14	3349	53.4	5288	2	AAV64093	Aav64093 Human pat
15	3349	53.4	5288	5	AAF32185	Aaf32185 Human pat
16	3349	53.4	5288	9	ACA62839	Aca62839 Human pat
17	3349	53.4	5288	10	ADE94223	Ade94223 Human ptc
18	3349	53.4	5288	10	ADH62730	Adh62730 Human pat
19	3349	53.4	5288	12	ADE48988	Ade48988 Human pat
20	3347	53.4	5288	6	ABA00374	Aba00374 Human pat
21	3337	53.2	5187	2	AAV21587	Aav21587 Precis co
22	3337	53.2	5187	2	AAV21589	Aav21589 Mouse pat
23	3337	53.2	5187	2	AAV64099	Aav64099 Precis co
24	3337	53.2	5187	2	AAV64092	Aav64092 Mouse pat
25	3337	53.2	5187	5	AAF32177	Aaf32177 Butterfly
26	3337	53.2	5187	5	AAF32180	Aaf32180 Murine pa
27	3337	53.2	5187	9	ACA62831	Aca62831 Full leng
28	3337	53.2	5187	9	ACA62834	Aca62834 Mouse pat
29	3337	53.2	5187	10	ADE94208	Ade94208 Peacock b
30	3337	53.2	5187	10	ADE94214	Ade94214 Murine pt
31	3337	53.2	5187	10	ADH62715	Adh62715 Butterfly
32	3337	53.2	5187	10	ADH62721	Adh62721 Mouse pat
33	3337	53.2	5187	12	ADE48979	Ade48979 Mouse pat
34	3337	53.2	5187	12	ADE48973	Ade48973 Butterfly
35	3337	53.2	5288	2	AAV21590	Aav21590 Human pat
36	3336	53.2	6568	2	AAV15949	Aav15949 Nevoid ba
37	3335	53.2	5187	2	AAT14218	Aat14218 Mouse pat
38	3331	53.1	5187	6	ABA00375	Aba00375 Mouse pat
39	3330	53.1	5187	6	ABA00376	Aba00376 Butterfly
40	3329	53.1	6568	6	ABL67232	Abl67232 Thyroid c
41	3329	53.1	6568	6	ABK84327	Abk84327 Human cDN
42	3173	50.6	7753	10	ADF81708	Adf81708 Leukaemia
43	3173	50.6	7753	10	ADF81706	Adf81706 Leukaemia
44	2797.5	44.6	2032	2	AAV69382	Aav69382 Human Pat
45	2003	31.9	3861	4	ABL04551	Abl04551 Drosophil

ALIGNMENTS

RESULT 1
AAZ31717
ID AAZ31717 standard; DNA; 4030 BP.
XX
AC AAZ31717;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human patched-2 coding sequence.
XX
KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
KW cell proliferation; cell differentiation; testicular cancer; gut disease;
KW degenerative disorder; nervous system disorder; Parkinson's disease;
KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
KW therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9953058-A1.
XX
PD 21-OCT-1999.
XX
PF 02-APR-1999; 99WO-US007417.
XX
PR 15-APR-1998; 98US-00060939.
XX
PA (GETH) GENENTECH INC.
XX

PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 1999-620428/53.
DR P-PSDB; AAY43261.
XX
PT New isolated human patched-2 gene, used to develop products for treating,
PT e.g. cancer and Alzheimer's disease.
XX
PS Claim 1; Fig 1; 124pp; English.
XX
CC This sequence encodes the human patched-2 (ptch-2) protein of the
CC invention. The patched-2 polypeptides are signalling molecules,
CC specifically for signalling and mediator molecules in the hedgehog (hh)
CC cascade which are involved in cell proliferation and differentiation.
CC They can be used for the treatment of disorders which are mediated at
CC least in part by Hh, especially Dhh, e.g. testicular cancer. They can
CC also be used for treating degenerative disorders of the nervous system,
CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou
CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
CC diseases, skin diseases, diseases of the testis (including infertility),
CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
CC osteoporosis. Antagonists or agonists of patched-2 may be used for
CC treating disorders or creating a desirable physiological condition
CC effected by blocking Hh signalling, especially Dhh signalling, e.g.
CC contraception or infertility treatment. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic animals
XX
SQ Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4030
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

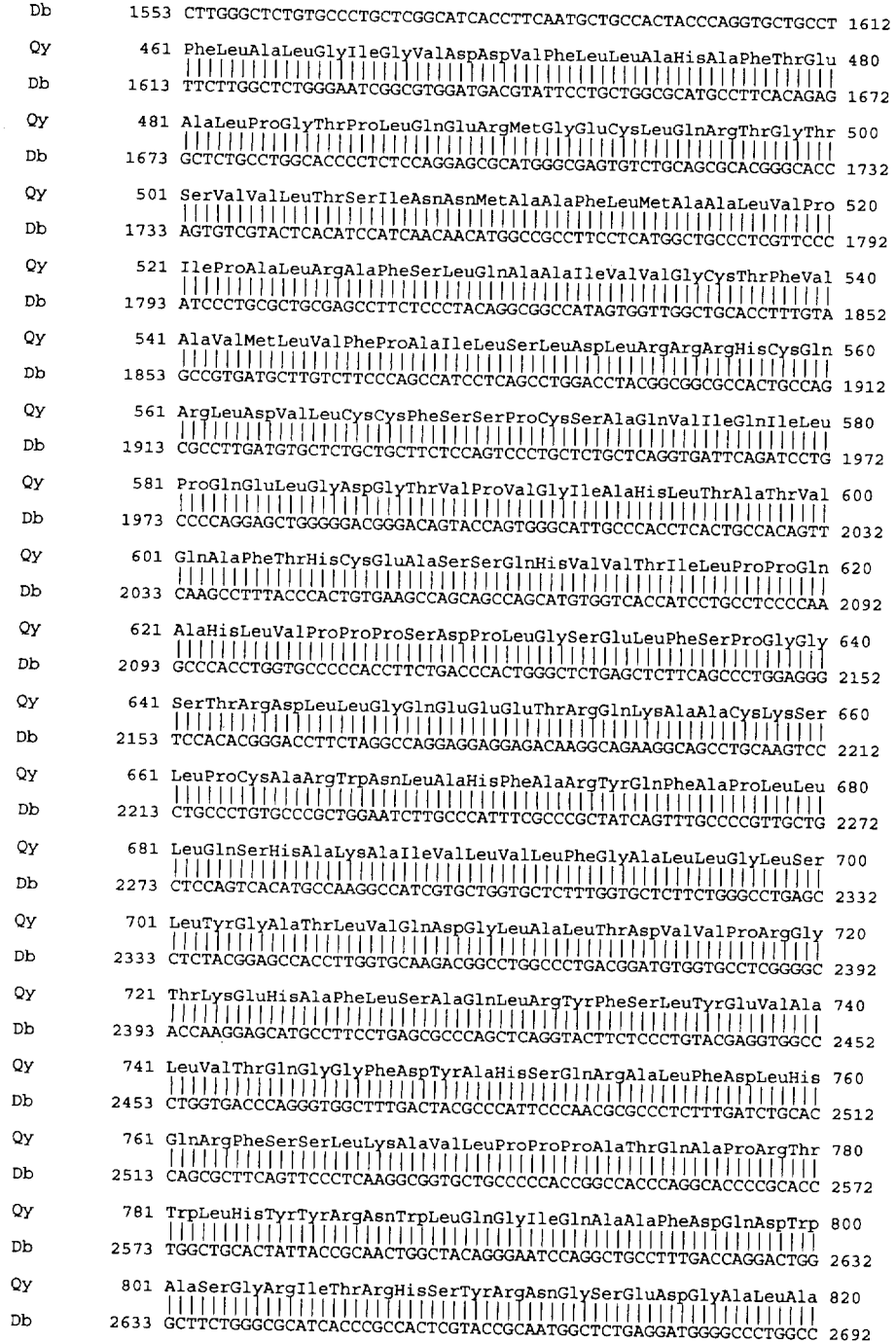
US-09-990-046-2 (1-1203) x AAZ31717 (1-4030)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGluGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972
Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572
Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632
Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752
Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872
Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932
Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992
Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db       2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052
Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db       3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112
Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db       3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172
Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db       3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232
Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db       3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292
Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db       3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352
Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db       3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412
Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db       3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472
Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db       3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532
Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db       3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592
Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db       3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652
Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db       3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712
Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db       3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772
Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832
Qy       1201 AlaThrGly 1203
Db       3833 GCCACTGGG 3841
```

RESULT 2
AAD31576
ID AAD31576 standard; cDNA; 4030 BP.
XX
AC AAD31576;
XX
DT 18-JUN-2002 (first entry)
XX

```
DE   Human patched-2 (Ptch-2) cDNA.
XX
KW   Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW   cytostatic; testicular cancer; hedgehog protein signalling; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             233. .3844
FT                   /*tag=  a
FT                   /product= "Human Ptch-2 protein"
XX
PN   US6348575-B1.
XX
PD   19-FEB-2002.
XX
PF   15-APR-1999;   99US-00293505.
XX
PR   15-APR-1998;   98US-0081884P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage F,  Carpenter DA;
XX
DR   WPI; 2002-215260/27.
DR   P-PSDB; AAE19829.
XX
PT   Native human patched-2 polypeptide for treating disorders caused by
PT   Hedgehog protein signaling such as testicular cancer, and for screening
PT   cDNA libraries.
XX
PS   Example 1; Fig 1; 82pp; English.
XX
CC   The invention relates to an isolated sequence comprising a native human
CC   patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC   and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC   cell proliferation and differentiation. The isolated sequence is useful
CC   for the treatment of disorders which are linked to Hedgehog, especially
CC   Desert hedgehog expression, such as testicular cancer. It may also be
CC   used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC   homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC   Hedgehog protein signalling. The present sequence is human patched-2
CC   (Ptch-2) cDNA
XX
SQ   Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0          Length:          4030
Score:                    6272.00    Matches:         1203
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0
DB:                       6          Gaps:            0

US-09-990-046-2 (1-1203) x AAD31576 (1-4030)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```


Db 1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992
Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052
Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112
Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472
Qy 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532
Qy 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db 3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592
Qy 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db 3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652
Qy 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712
Qy 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

```
Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy       1201 AlaThrGly 1203
             |||||||||
Db       3833 GCCACTGGG 3841

RESULT 3
ABX15919
ID   ABX15919 standard; DNA; 4030 BP.
XX
AC   ABX15919;
XX
DT   02-APR-2003  (first entry)
XX
DE   Human cDNA for patched-2 with vector sequences.
XX
KW   Human; patched-2; Dhh signalling; proliferation; differentiation; ds;
KW   chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW   basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW   Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW   Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW   bone disease; skin disease; testicular disease; ulcer; lung disease;
KW   pancreatic disease; diabetes; osteoporosis; SNP;
KW   single nucleotide polymorphism; desert hedgehog.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .212
FT                   /*tag=  a
FT                   /note= "Vector sequence"
FT   CDS             233. .3844
FT                   /*tag=  b
FT                   /product= "Patched-2"
FT   variation       replace(3925,T)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   misc_feature    3997. .4030
FT                   /*tag=  d
FT                   /note= "Vector sequence"
XX
PN   US2002156245-A1.
XX
PD   24-OCT-2002.
XX
PF   20-NOV-2001; 2001US-00990046.
XX
PR   15-APR-1998;   98US-0081884P.
PR   15-APR-1999;   99US-00293505.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage FJ,  Carpenter DA;
XX
DR   WPI; 2003-182650/18.
DR   P-PSDB; ABG74104.
XX
PT   New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT   treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT   e.g., testicular cancer.
XX
PS   Example 1; Fig 1; 85pp; English.
XX
CC   The invention relates to a new isolated nucleic acid encoding a
CC   polypeptide having patched-2 biological activity, comprises DNA having at
CC   least 95% sequence identity with a DNA molecule or its complement
CC   encoding: (a) a human patched-2 polypeptide comprising the sequence
CC   ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC   Deposit No. 209778 designation). Also included are a vector comprising
CC   the nucleic acid, a host cell transformed with the vector, a process for
CC   producing patched-2 polypeptides, an isolated native sequence of human
CC   patched-2 polypeptide, a chimaeric molecule comprising the vertebrate
CC   patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC   patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC   hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC   patched-2 that stimulates or enhances the normal functioning of patched-2
CC   in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC   and diagnosing to determine whether a particular disorder is modulated
CC   The nucleic acid is useful for manufacturing a medicament for diagnosing
CC   or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC   basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC   Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC   Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC   diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC   diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC   Patched-2 may also be used to develop male contraceptives. The gene for
CC   Patched-2 is located on human chromosome 1p33-34. The present sequence is
CC   the human cDNA for patched-2 (along with some vector derived sequences)
XX
SQ   Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0                 Length:          4030
Score:                    6272.00           Matches:         1203
Percent Similarity:       100.00%           Conservative:    0
Best Local Similarity:    100.00%           Mismatches:      0
Query Match:              100.00%           Indels:          0
DB:                       8                 Gaps:            0

US-09-990-046-2 (1-1203) x ABX15919 (1-4030)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db        893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db        953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012
Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072
Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132
Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312
Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372
Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432
Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492
Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552
Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db       1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db       1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672
Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db       1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db       1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792
Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db       1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy        541 AlaValMetLeuValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572
Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632
Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752
Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872
Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932
Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992
Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db       2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052
```

```
Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy      1201 AlaThrGly 1203
Db      3833 GCCACTGGG 3841
```

RESULT 4
AAX89478
ID AAX89478 standard; cDNA; 4391 BP.
XX
AC AAX89478;
XX
DT 03-DEC-1999 (first entry)
XX
DE Human ptc-2 cDNA.
XX
KW Patched-2; ptc-2; human; hedgehog receptor; nootropic; neuroprotective;
KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
KW graft; transplant; treatment; nervous system injury; chemical injury;
KW vasal injury; infection; inflammatory; tumor-induced injury; ageing;
KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
KW Parkinson's disease; Huntingdon's chorea; amylotrophic lateral sclerosis;
KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
KW lesion-induced death; neuron regeneration; damage repair; skeletal;
KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
KW prosthetic cartilage device; spermatogenesis; fertility enhancer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 297. .3908
FT /*tag= a
FT /product= "ptc-2"
XX
PN WO9929854-A1.
XX
PD 17-JUN-1999.
XX
PF 08-DEC-1998; 98WO-US026009.
XX
PR 08-DEC-1997; 97US-0067940P.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Bumcrot DA;
XX
DR WPI; 1999-561298/47.
DR P-PSDB; AAY28444.
XX
PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
PT prevention and/or reduction of the severity of neurological conditions.
XX
PS Claim 2; Page 66-72; 80pp; English.
XX
CC This invention describes a novel recombinantly produced human patched-2
CC (ptc-2) polypeptide which has nootropic, neuroprotective, cardiant,
CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
CC protein is a hedgehog receptor and is therefore capable of modulating
CC hedgehog signalling, and so affect a number of hedgehog-mediated
CC biological activities. The human patched-2 (ptc-2) protein can be used to
CC screen for modulators, antagonists and agonists, which are likely to play
CC an important role in the modulation of cellular proliferation and
CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
CC tissues during disease states. Modulators of ptc-2 protein can be used
CC for in vivo reformation of tissue; to improve grafting and morphology of
CC transplanted tissue; for the treatment, prevention and/or reduction of
CC the severity of neurological conditions deriving from: injury to the
CC nervous system including traumatic injury, chemical injury, vasal injury
CC and deficits (such as ischemia resulting from stroke), together with
CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
CC system including Alzheimer's disease; chronic neurodegenerative diseases
CC of the nervous system including Parkinson's disease, Huntingdon's chorea,
CC amylotrophic lateral sclerosis, as well as spinocerebellar degenerations;
CC and chronic immunological diseases of the nervous system including
CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
CC of autonomic disorders of the peripheral nervous system, including
CC disorders affecting the innervation of smooth muscle and endocrine
CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
CC Antagonists of ptc-2 protein can be used to prevent differentiation of
CC cells in culture, as well as for treatment of chronic pain syndromes.
CC Agonists may be used to rescue neurons from lesion-induced death as well
CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)
CC infection, metabolic disease, nutritional deficiency, toxic agents, and
CC so on. ptc-2 therapeutics may also be used for the repair of central and
CC peripheral nerve damage, for repair and regeneration of non-neuronal
CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
CC for generation of prosthetic cartilage devices, and to induce
CC spermatogenesis and as fertility enhancers. This sequence encodes the
CC human ptc-2 protein described in the invention
XX
SQ Sequence 4391 BP; 769 A; 1475 C; 1224 G; 923 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4391
Score:	6248.00	Matches:	1200
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	2	Gaps:	0

US-09-990-046-2 (1-1203) x AAX89478 (1-4391)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916

Qy        541 AlaValMetLeuValProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336
```

```
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396

Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456

Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516

Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576

Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996

Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db       3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db       3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db       3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db       3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db       3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db       3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db       3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db       3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db       3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db       3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db       3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db       3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db       3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db       3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy       1201 AlaThrGly 1203
Db       3897 GCCACTGGG 3905
```

```
RESULT 5
AAA09081
ID   AAA09081 standard; cDNA; 3453 BP.
XX
AC   AAA09081;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human patched-like gene (PTCH2) coding sequence.
XX
KW   Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
KW   familial adenomatous polyposis; hMom1; Michelin Tire Baby Syndrome;
KW   sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW   basal cell carcinoma; gene therapy; chromosome 1p32-35; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             13. .3453
FT                   /*tag=  a
XX
PN   WO200020037-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-SE001784.
XX
PR   06-OCT-1998;   98SE-00003393.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Zaphiropoulos PG,  Unden AB,  Toftgard R,  Rahnama F;
PI   Hollingsworth RE;
XX
DR   WPI; 2000-303645/26.
DR   P-PSDB; AAY92225.
```

XX
PT Isolated human protein capable of participating in human patched
PT gene/Sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX
PS Claim 4; Page 45; 55pp; English.
XX
CC This cDNA is derived from the novel human patched 2 gene (PTCH2), which
CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
CC D1S211 and WI1404 as closest flanking markers and with an estimated
CC localisation 5.5 cR from D1S443. This region is often lost by LOH in
CC various different tumour types, such as neuroblastoma, melanoma and
CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
CC gene in this region. It is also a candidate gene for involvement in
CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
CC hMom1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
CC exist (see AAA09082-84). PTCH2 is capable of participating in the human
CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
CC development and/or carcinogenesis. The isolated human protein is useful
CC as a medicament for the treatment of a condition involving tumours such
CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
CC therapy, and for use as a probe, primer or a diagnostic agent
XX
SQ Sequence 3453 BP; 600 A; 1135 C; 989 G; 729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3453
Score:	5911.00	Matches:	1139
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	3
Query Match:	94.24%	Indels:	0
DB:	3	Gaps:	0

US-09-990-046-2 (1-1203) x AAA09081 (1-3453)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 72

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 132

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 192

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 252

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 312

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 372

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 432

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 492

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        493 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 552

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 612

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 672

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 732

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 792

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 852

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 912

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 972

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1032

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1092

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1152

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1212

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1272

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1332

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1392

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1452

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1512

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1572

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1573 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1632

Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

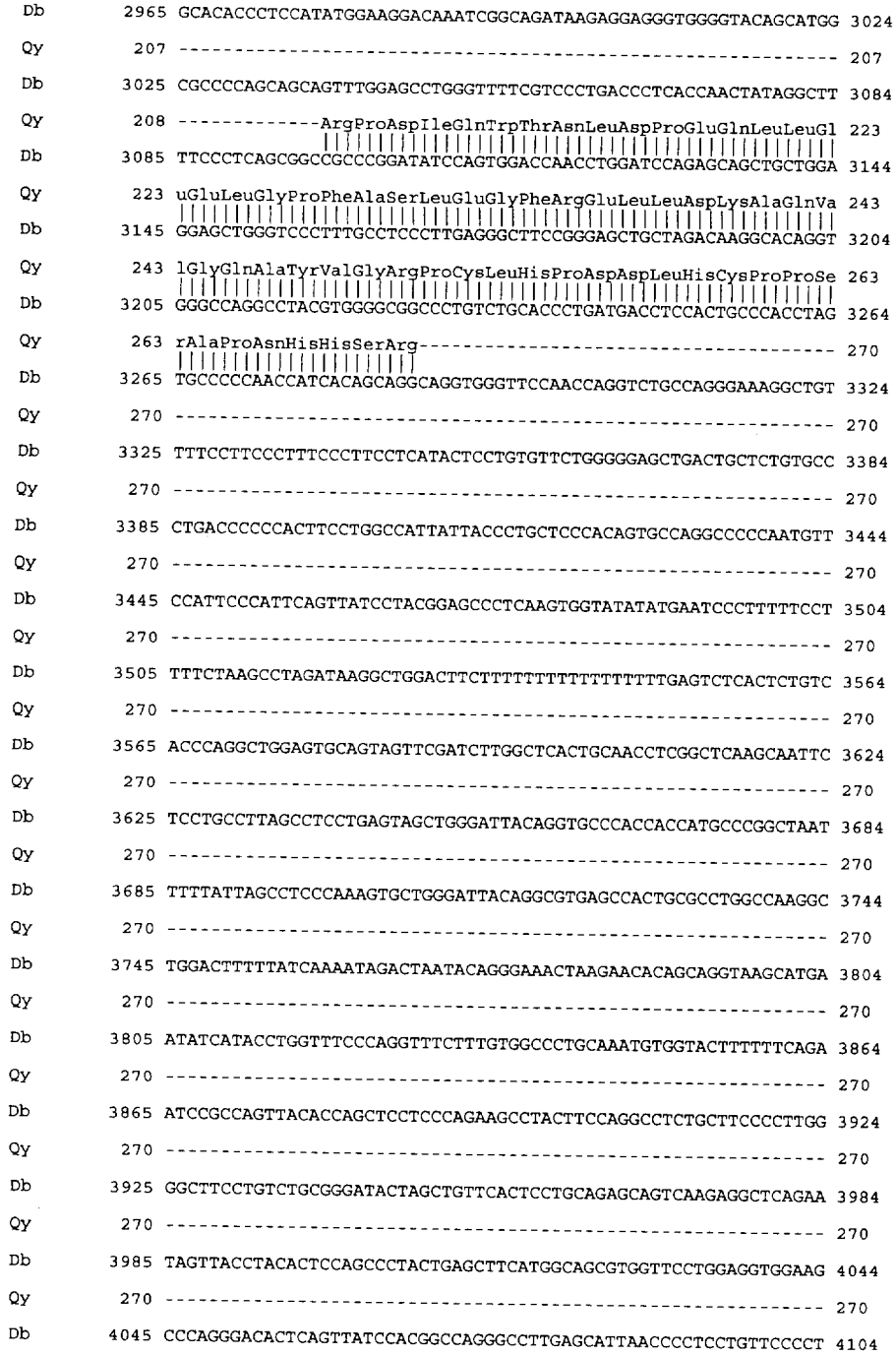
```
Db       1633 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1692
Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1693 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1752
Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1753 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1812
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       1813 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1872
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       1873 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1932
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       1933 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1992
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       1993 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2052
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2053 CTCCAGTCACATGCTAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2112
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2113 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2172
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2173 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2232
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2233 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2292
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2293 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2352
Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2353 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2412
Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2413 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2472
Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2473 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCTTCTGGATTTCAGCCAGCTGACC 2532
Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2533 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2592
Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2593 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2652
Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2653 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACTTTCGCATCCCG 2712
Qy        901 ProAlaGlnProLeuGluPheAlaGlnProProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2713 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2772

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db       2773 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2832
Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db       2833 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2892
Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db       2893 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2952
Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db       2953 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3012
Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db       3013 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3072
Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db       3073 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3132
Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db       3133 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3192
Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db       3193 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3252
Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db       3253 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3312
Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db       3313 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3372
Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db       3373 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3432
Qy       1141 LeuArg 1142
Db       3433 CTTAGG 3438
```

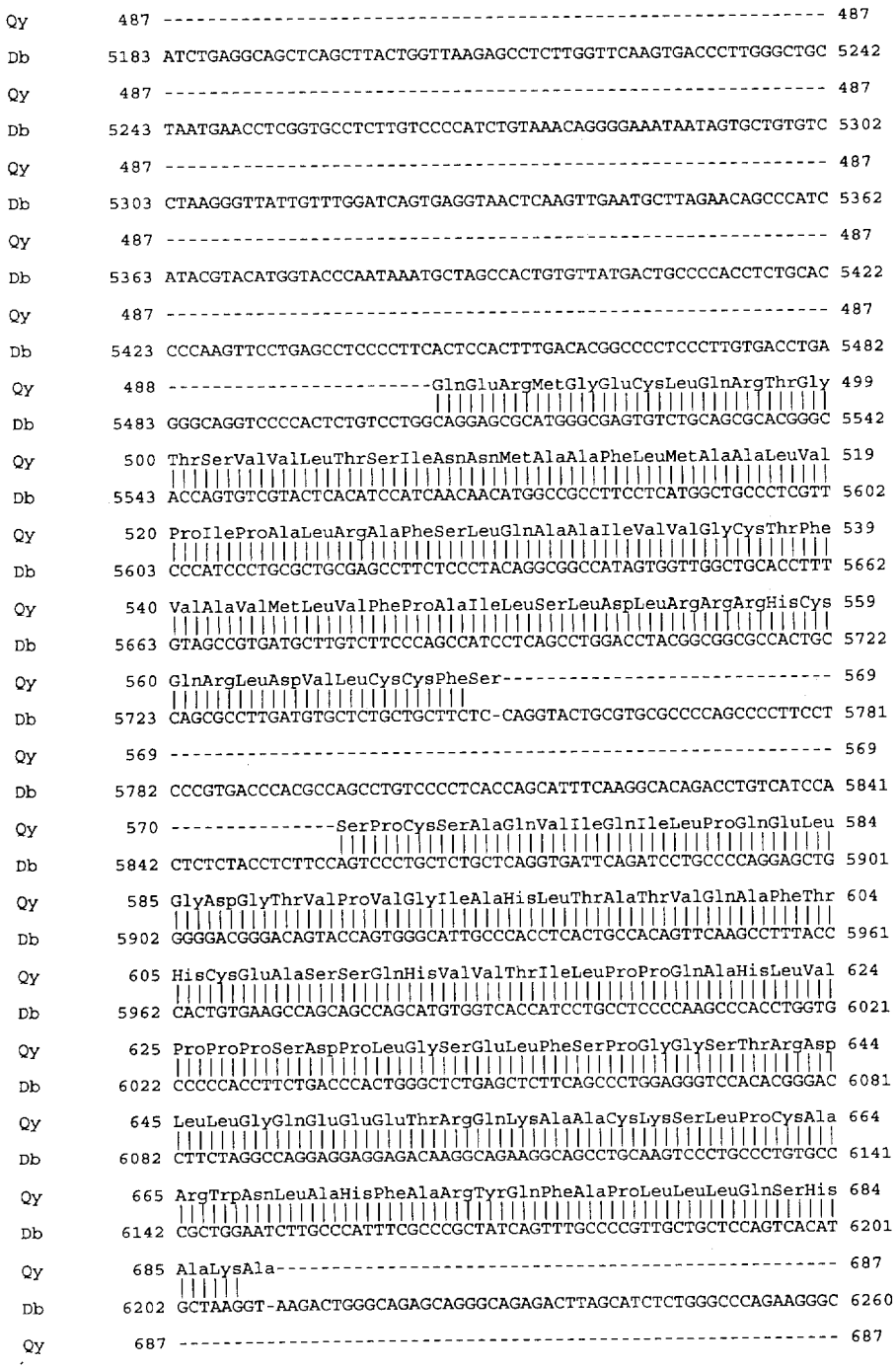
RESULT 6
AAA09084
ID AAA09084 standard; DNA; 12886 BP.
XX
AC AAA09084;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human patched-like gene (PTCH2) genomic DNA.
XX
KW Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
KW familial adenomatous polyposis; hMom1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW basal cell carcinoma; gene therapy; chromosome 1p32-35; ds.
XX
OS Homo sapiens.
XX

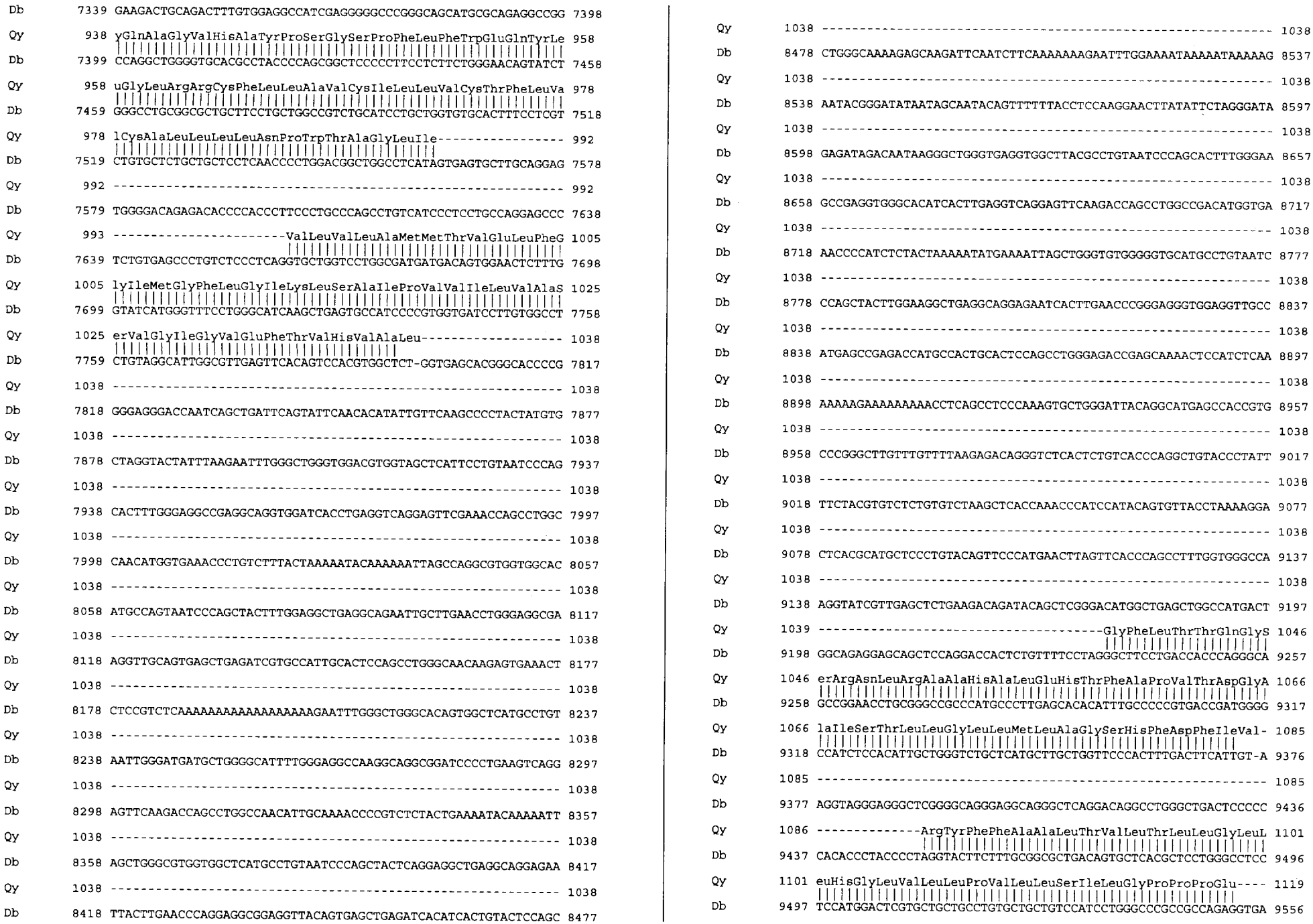
FH	Key	Location/Qualifiers
FT	exon	1. .290
FT		/*tag= c
FT		/number= 1
FT	CDS	219. .12033
FT		/*tag= a
FT		/product= "PTCH2"

```
FT   CDS             219. .10206
FT                   /*tag= b
FT                   /product= "splice_variant"
FT   intron          291. .1109
FT                   /*tag= d
FT   exon            1110. .1302
FT                   /*tag= e
FT                   /number= 2
FT   intron          1303. .1795
FT                   /*tag= f
FT   exon            1796. .1986
FT                   /*tag= g
FT                   /number= 3
FT   intron          1987. .2093
FT                   /*tag= h
FT   exon            2094. .2162
FT                   /*tag= i
FT                   /number= 4
FT   intron          2163. .2339
FT                   /*tag= j
FT   exon            2340. .2431
FT                   /*tag= k
FT                   /number= 5
FT   intron          2432. .3093
FT                   /*tag= l
FT   exon            3094. .3289
FT                   /*tag= m
FT                   /number= 6
FT   intron          3290. .4108
FT                   /*tag= n
FT   exon            4109. .4231
FT                   /*tag= o
FT                   /number= 7
FT   intron          4232. .4378
FT                   /*tag= p
FT   exon            4379. .4586
FT                   /*tag= q
FT                   /number= 8
FT   intron          4587. .4605
FT                   /*tag= r
FT   exon            4607. .4738
FT                   /*tag= s
FT                   /number= 9
FT   intron          4739. .4827
FT                   /*tag= t
FT   exon            4828. .4983
FT                   /*tag= u
FT                   /number= 10
FT   intron          4984. .5065
FT                   /*tag= v
FT   exon            5066. .5158
FT                   /*tag= w
FT                   /number= 11
FT   intron          5159. .5509
FT                   /*tag= x
FT   exon            5510. .5754
FT                   /*tag= y
FT                   /number= 12
FT   intron          5755. .5858
FT                   /*tag= z
FT   exon            5859. .6207
FT                   /*tag= aa
FT                   /number= 13
FT   intron          6208. .6335
FT                   /*tag= ab
FT   exon            6336. .6648
FT                   /*tag= ac
FT                   /number= 14
FT   intron          6649. .6740
FT                   /*tag= ad
FT   exon            6741. .6882
FT                   /*tag= ae
FT                   /number= 15
FT   intron          6883. .6966
FT                   /*tag= af
FT   exon            6967. .7147
FT                   /*tag= ag
FT                   /number= 16
FT   intron          7148. .7280
FT                   /*tag= ah
FT   exon            7281. .7561
FT                   /*tag= ai
FT                   /number= 17
FT   intron          7562. .7661
FT                   /*tag= aj
FT   exon            7662. .7799
FT                   /*tag= ak
FT                   /number= 18
FT   intron          7800. .9235
FT                   /*tag= al
FT   exon            9236. .9378
FT                   /*tag= am
FT                   /number= 19
FT   intron          9379. .9452
FT                   /*tag= an
FT   exon            9453. .9552
FT                   /*tag= ao
FT                   /number= 20
FT   intron          9553. .9951
FT                   /*tag= ap
FT   exon            9952. .10206
FT                   /*tag= ar
FT                   /number= 21a
FT                   /note= "alternate splice variant"
FT   exon            9952. .10019
FT                   /*tag= aq
FT                   /number= 21
FT   intron          10020. .12017
FT                   /*tag= as
FT   exon            12018. .12886
FT                   /*tag= at
FT                   /number= 22
XX
PN   WO200020037-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-SE001784.
XX
PR   06-OCT-1998;   98SE-00003393.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Zaphiropoulos PG,  Unden AB,  Toftgard R,  Rahnama F;
PI   Hollingsworth RE;
XX
DR   WPI; 2000-303645/26.
DR   P-PSDB; AAY92225, AAY92703.
XX
PT   Isolated human protein capable of participating in human patched
PT   gene/Sonic hedgehog pathway during embryonic development is used in
PT   medicament for treatment of condition involving tumors such as basal cell
PT   carcinoma.
XX
PS   Claim 5; Page 46-49; 55pp; English.
XX
CC   This genomic DNA comprises the novel human patched 2 gene (PTCH2), which
CC   has been localised by radiation hybrid mapping to chromosome 1p32-35 with
CC   D1S211 and WI1404 as closest flanking markers and with an estimated
CC   localisation 5.5 cR from D1S443. A splice variant exists which is
CC   generated by 2 forms of exon 21. This region is often lost by LOH in
CC   various different tumour types, such as neuroblastoma, melanoma and
CC   breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
CC   gene in this region. It is also a candidate gene for involvement in
CC   familial melanoma CMM1, modifier locus for familial adenomatous polyposis
```

```
CC   hMom1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
CC   exist (see AAA09082-84). PTCH2 is capable of participating in the human
CC   patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
CC   development and/or carcinogenesis. The isolated human protein is useful
CC   as a medicament for the treatment of a condition involving tumours such
CC   as BCC (basal cell carcinoma). The nucleic acid is useful in gene
CC   therapy, and for use as a probe, primer or a diagnostic agent
XX
SQ   Sequence 12886 BP; 2789 A; 3817 C; 3472 G; 2807 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:                0              Length:          12886
Score:                    4682.50        Matches:         1166
Percent Similarity:       38.40%         Conservative:    1
Best Local Similarity:    38.37%         Mismatches:      13
Query Match:              74.66%         Indels:          1869
DB:                       3              Gaps:            20

US-09-990-046-2 (1-1203) x AAA09084 (1-12886)

Qy         24 GlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeu 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 CAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTCCAGGGCCTG 1166

Qy         44 LeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeu 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 CTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTTCTGGGACTG 1226

Qy         64 LeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGlu 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 TTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACAAACTTGGAA 1286

Qy         84 GlnLeuTrpValGlu---------------------------------------------- 88
              ||||||||||||||
Db       1287 CAGCTCTGGGTAGAAGGTAAGTTGTGGACACTGGCCATAGCTGCTCAGGTATGGTGAGCC 1346

Qy         88 ------------------------------------------------------------ 88

Db       1347 CAAGACAAGAACGGGGTGAGGAGCTGGCTACTGAGCTCTAGCAGGCCTGGCCCTGGGGCT 1406

Qy         88 ------------------------------------------------------------ 88

Db       1407 GGAGGGTCACCTGCTGGCCAGAGTCCTACACCTGGGCATCTAGGAACACCGTTCCCTCCC 1466

Qy         88 ------------------------------------------------------------ 88

Db       1467 ACAACCATAAATGGACATCTGCAGATGTTAGACCTTGTGAATTGGGTGTATAGAATATTT 1526

Qy         88 ------------------------------------------------------------ 88

Db       1527 GTCTGTGATTTTGCTTAAGCCCTAGACCACACAAGAAATCCGCAGAGCCACACAACCGAG 1586

Qy         88 ------------------------------------------------------------ 88

Db       1587 GCTTCTCCACTTCCCTGGCAGAGCTCCAGGACCCAGAAGCCTGGGGAGTCGGCCTGGGCC 1646

Qy         88 ------------------------------------------------------------ 88

Db       1647 ATGACCAGGCCCTCAGGGATAAGGCAGGGACTCCTCTCTGCCGCACCTCTCCCACTTGTC 1706

Qy         88 ------------------------------------------------------------ 88

Db       1707 TGGGGAGGCCTCAGAGTTAGAAGCCCCCTTCGCAAGTTCTGACCCGCCTAGGCCCTTTCC 1766

Qy         89 ----------------------------ValGlySerArgValSerGlnGluLeuHisTy 99
                                          ||||||||||||||||||||||||||||||
Db       1767 CCCCCAGCTTTCTCTGTTTGCTCTGGCAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTA 1826

Qy         99 rThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAl 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1827 CACCAAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGC 1886

Qy        119 aArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAl 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1887 ACGCCAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGC 1946

Qy        139 aLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSer---------------- 153
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1947 CCTCACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGGT-GAGTCTGGCTGAGCCCC 2005

Qy        153 ------------------------------------------------------------ 153

Db       2006 TGAGCAGCTGGGGGCGAGGCGTGCTGTGGGGGTTCTGGAGTGGGAATCCCCTTCTTCTGC 2065

Qy        154 ------------------------------TrpAspLeuAsnLysIleCysTyrLysSe 163
                                            ||||||||||||||||||||||||||||||
Db       2066 TGATCTCCTATGCCCCTGGCTATTGCAGTCCTGGGATTTGAACAAAATCTGCTACAAGTC 2125

Qy        163 rGlyValProLeuIleGluAsnGlyMetIleGlu-------------------------- 174
              ||||||||||||||||||||||||||||||||
Db       2126 AGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGGTAAGTGTCCTGAGAGGGAGTAG 2185

Qy        174 ------------------------------------------------------------ 174

Db       2186 AGGCAGAACTTTTTCTGTAGCGTGGGAGGACTCAGAGACCGAGCAAGCCCCACAGCCTGC 2245

Qy        174 ------------------------------------------------------------ 174

Db       2246 AATCTGCCCCCTTAAAACTAAGGAGGGGGATTGCAGAGGGCATCCTACAAAGGTTGTGGG 2305

Qy        175 ----------------------------Trp---MetIleGluLysLeuProCysVa 184
                                           |||   ||||||||||||||||||||||
Db       2306 GCAGGACTGACGTGGCCCGGGGTATCCCTGGCAGATGATTGAGAAGCTGTTTCCGTGCGT 2365

Qy        184 lIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlySerAlaTy 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGGGGCTCCGCCTA 2425

Qy        204 rLeuProGly--------------------------------------------------- 207
              |||||||
Db       2426 CCTGCCGTG-AGTGCCACTCCTGGGGCCCTGCTTCATCTCCCGCTGGGGACTCTCCCAGC 2484

Qy        207 ------------------------------------------------------------ 207

Db       2485 AGAAAGGAGGGGTCTGGGGAATGAGGATGATCAAAACCTTACCAAGGTCCTAATTACCTC 2544

Qy        207 ------------------------------------------------------------ 207

Db       2545 CCAGGCCAGGAACAGAGAGCATGGGCTTCCCCAAGGCTCTCTCCACATCCTCCTTCTCTT 2604

Qy        207 ------------------------------------------------------------ 207

Db       2605 TCCCTCTCAAGGAAGGAAGACCTGACTTATTTACACAAAACTAAACACAAAGATCTGTAA 2664

Qy        207 ------------------------------------------------------------ 207

Db       2665 GATCTGAGCAAAGGAGAAAAAGATCCCCACAAAGAGGCTTTGCTGGGGGAAATTACCTAG 2724

Qy        207 ------------------------------------------------------------ 207

Db       2725 GTGTTTGCTAAGCCATTGCCCAGGCCAGAAAGAAAACCTGCTACAGGCATGTGCCTGCTG 2784

Qy        207 ------------------------------------------------------------ 207

Db       2785 GTTGTATATTAGAACCAAGCACACAGCTTGGTAAGGAACTCAGTGGGGCCTTTCTGGGCC 2844

Qy        207 ------------------------------------------------------------ 207

Db       2845 CTTTCTATGTATTAGGTAACCCTGCCCTGATATTCGTCTCAGCCCCTTGTACTCTTCTAC 2904

Qy        207 ------------------------------------------------------------ 207

Db       2905 AGCTCACTGTAGCACCCTGGTGGGCCCATGCAGCCTGGCAGTTCTGAGAAGCTGAGGCTT 2964

Qy        207 ------------------------------------------------------------ 207
```


Db 2965 GCACACCCTCCATATGGAAGGACAAATCGGCAGATAAGAGGAGGGTGGGGTACAGCATGG 3024
Qy 207 ---------- 207
Db 3025 CGCCCCAGCAGCAGTTTGGAGCCTGGGTTTTCGTCCCTGACCCTCACCAACTATAGGCTT 3084
Qy 208 ----------ArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGl 223
Db 3085 TTCCCTCAGCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAGCTGCTGGA 3144
Qy 223 uGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnVa 243
Db 3145 GGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAGGCACAGGT 3204
Qy 243 lGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCysProProSe 263
Db 3205 GGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGCCCACCTAG 3264
Qy 263 rAlaProAsnHisHisSerArg---------- 270
Db 3265 TGCCCCCAACCATCACAGCAGGCAGGTGGGTTCCAACCAGGTCTGCCAGGGAAAGGCTGT 3324
Qy 270 ---------- 270
Db 3325 TTTCCTTCCCTTTCCCTTCCTCATACTCCTGTGTTCTGGGGGAGCTGACTGCTCTGTGCC 3384
Qy 270 ---------- 270
Db 3385 CTGACCCCCCACTTCCTGGCCATTATTACCCTGCTCCCACAGTGCCAGGCCCCCAATGTT 3444
Qy 270 ---------- 270
Db 3445 CCATTCCCATTCAGTTATCCTACGGAGCCCTCAAGTGGTATATATGAATCCCTTTTTCCT 3504
Qy 270 ---------- 270
Db 3505 TTTCTAAGCCTAGATAAGGCTGGACTTCTTTTTTTTTTTTTTTTGAGTCTCACTCTGTC 3564
Qy 270 ---------- 270
Db 3565 ACCCAGGCTGGAGTGCAGTAGTTCGATCTTGGCTCACTGCAACCTCGGCTCAAGCAATTC 3624
Qy 270 ---------- 270
Db 3625 TCCTGCCTTAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCACCACCATGCCCGGCTAAT 3684
Qy 270 ---------- 270
Db 3685 TTTTATTAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGCCTGGCCAAGGC 3744
Qy 270 ---------- 270
Db 3745 TGGACTTTTTATCAAAATAGACTAATACAGGGAAACTAAGAACACAGCAGGTAAGCATGA 3804
Qy 270 ---------- 270
Db 3805 ATATCATACCTGGTTTCCCAGGTTTCTTTGTGGCCCTGCAAATGTGGTACTTTTTTCAGA 3864
Qy 270 ---------- 270
Db 3865 ATCCGCCAGTTACACCAGCTCCTCCCAGAAGCCTACTTCCAGGCCTCTGCTTCCCCTTGG 3924
Qy 270 ---------- 270
Db 3925 GGCTTCCTGTCTGCGGGATACTAGCTGTTCACTCCTGCAGAGCAGTCAAGAGGCTCAGAA 3984
Qy 270 ---------- 270
Db 3985 TAGTTACCTACACTCCAGCCCTACTGAGCTTCATGGCAGCGTGGTTCCTGGAGGTGGAAG 4044
Qy 270 ---------- 270
Db 4045 CCCAGGGACACTCAGTTATCCACGGCCAGGGCCTTGAGCATTAACCCCTCCTGTTCCCCT 4104
Qy 271 -Gln-AlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysP 290
Db 4105 CCAGGGCTCCCAATGTGGCTCACGAGCTGAGTGGGGGCTGCCATGGCTTCTCCCACAAAT 4164
Qy 290 heMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluL 310
Db 4165 TCATGCACTGGCAGGAGGAATTGCTGCTGGGAGGCATGGCCAGAGACCCCCAAGGAGAGC 4224
Qy 310 euLeu---------- 311
Db 4225 TGCTGAGGTAGGGTCTCCTCTGGGAGTTGGTGAGGGGACTCTGTTCATGAGAACCCATAC 4284
Qy 311 ---------- 311
Db 4285 TGTAATGCCAGGCAGCTCTGGCAAAAGGCCCTTCACATCCCTCACCAGGTGTTTGGGCCA 4344
Qy 312 ----------ArgAlaGluAlaLeuGlnSerThrPheL 321
Db 4345 GCTCTGACCCCTGGTTCTCCCACACCCCCACCAGGGCAGAGGCCCTGCAGAGCACCTTCT 4404
Qy 321 euLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAspI 341
Db 4405 TGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGACA 4464
Qy 341 leGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArg------- 358
Db 4465 TTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTGC 4524
Qy 358 ---------- 358
Db 4525 AGGTCGGTATGGACAAGGACAAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 4584
Qy 359 ----------PheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnG 374
Db 4585 CCTATCCACCCTGTTTCTC-CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGC 4643
Qy 374 lnIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValS 394
Db 4644 AGATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCA 4703
Qy 394 erAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu---------- 406
Db 4704 GTGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGT-GGGTCTTGCACCTGGCACCTTG 4762
Qy 406 ---------- 406
Db 4763 CCCCCACCCCACCTCCAACCAGTGCCCACCCTGGGAGCCCCTGAGACTGCCCTTTCCCCC 4822
Qy 407 --------AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlyS 424
Db 4823 CACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTT 4882
Qy 424 erValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuC 444
Db 4883 CCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCT 4942
Qy 444 ysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------- 456
Db 4943 GTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGG 5002
Qy 456 ---------- 456
Db 5003 CAGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTC 5062
Qy 457 GlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHis 476
Db 5063 CAGGTGCTGCCCTTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCAT 5122
Qy 477 AlaPheThrGluAlaLeuProGlyThrProLeu---------- 487
Db 5123 GCCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTC 5182


Qy 487 ---------- 487
Db 5183 ATCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCCTTGGGCTGC 5242
Qy 487 ---------- 487
Db 5243 TAATGAACCTCGGTGCCTCTTGTCCCCATCTGTAAACAGGGGAAATAATAGTGCTGTGTC 5302
Qy 487 ---------- 487
Db 5303 CTAAGGGTTATTGTTTGGATCAGTGAGGTAACTCAAGTTGAATGCTTAGAACAGCCCATC 5362
Qy 487 ---------- 487
Db 5363 ATACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCAC 5422
Qy 487 ---------- 487
Db 5423 CCCAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGA 5482
Qy 488 ----------GlnGluArgMetGlyGluCysLeuGlnArgThrGly 499
Db 5483 GGGCAGGTCCCCACTCTGTCCTGGCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGC 5542
Qy 500 ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuVal 519
Db 5543 ACCAGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTT 5602
Qy 520 ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe 539
Db 5603 CCCATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTT 5662
Qy 540 ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCys 559
Db 5663 GTAGCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGC 5722
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 5723 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCGTGCGCCCCAGCCCCTTCCT 5781
Qy 569 ---------- 569
Db 5782 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 5841
Qy 570 ----------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 5842 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 5901
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 5902 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 5961
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 5962 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 6021
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 6022 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 6081
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 6082 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 6141
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 6142 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 6201
Qy 685 AlaLysAla---------- 687
Db 6202 GCTAAGGT-AAGACTGGGCAGAGCAGGGCAGAGACTTAGCATCTCTGGGCCCAGAAGGGC 6260
Qy 687 ---------- 687
Db 6261 AGAGAGGGCTTAGTCCACTGCCTGAGGGGCTGGGGGCAGCCCTGGGGTCTCCAGCTTAGT 6320
Qy 688 ----------IleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeu 701
Db 6321 TGCTACATCCCGCAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTC 6380
Qy 702 TyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThr 721
Db 6381 TACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACC 6440
Qy 722 LysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeu 741
Db 6441 AAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTG 6500
Qy 742 ValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGln 761
Db 6501 GTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAG 6560
Qy 762 ArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrp 781
Db 6561 CGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGG 6620
Qy 782 LeuHisTyrTyrArgAsnTrpLeuGlnGlyIle---------- 792
Db 6621 CTGCACTATTACCGCAACTGGCTACAGGGTGA-GAGGCGAGGAGACGGGCAGGGAGGGGT 6679
Qy 792 ---------- 792
Db 6680 GCTGCAGGGAGAAACGCCCTGGGGCCACCAGCTAATAGAACCCTATCCTGGTCTCCCCCA 6739
Qy 793 ------GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyr 810
Db 6740 GGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGCATCACCCGCCACTCGAC- 6798
Qy 811 ArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAla 830
Db 6799 CGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTCATCCAGACTGGAGACGCC 6858
Qy 831 GlnGluProLeuAspPheSer---------- 837
Db 6859 CAGGAGCTTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAGGGGTCCACTAGTACAGGG 6918
Qy 838 ----------GlnLeuThrThrArg 842
Db 6919 GCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCTCTGCAGCTGACCACAAGG 6978
Qy 843 LysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrVal 862
Db 6979 AAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTGACCGTG 7038
Qy 863 TrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProPro 882
Db 7039 TGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCCCCACCT 7098
Qy 883 ProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArg---------- 898
Db 7099 CCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACTTTCGCAGTGAGTCTTGG 7158
Qy 898 ---------- 898
Db 7159 GGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCTGAGCCTGAGGCCCTGCCC 7218
Qy 898 ---------- 898
Db 7219 ACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTCCCTTCCCCTCCCCTCCAC 7278
Qy 899 -IleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGl 918
Db 7279 AGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCTTTCCTGCTGCGTGGCCTCCA 7338
Qy 918 nLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGl 938


Db 7339 GAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGG 7398
Qy 938 yGlnAlaGlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLe 958
Db 7399 CCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCT 7458
Qy 958 uGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuVa 978
Db 7459 GGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGT 7518
Qy 978 lCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIle---------- 992
Db 7519 CTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGAGTGCTTGCAGGAG 7578
Qy 992 ---------- 992
Db 7579 TGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCATCCCTCCTGCCAGGAGCCC 7638
Qy 993 ----------ValLeuValLeuAlaMetMetThrValGluLeuPheG 1005
Db 7639 TCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTG 7698
Qy 1005 lyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaS 1025
Db 7699 GTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTGATCCTTGTGGCCT 7758
Qy 1025 erValGlyIleGlyValGluPheThrValHisValAlaLeu---------- 1038
Db 7759 CTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCT-GGTGAGCACGGGCACCCCG 7817
Qy 1038 ---------- 1038
Db 7818 GGGAGGGACCAATCAGCTGATTCAGTATTCAACACATATTGTTCAAGCCCCTACTATGTG 7877
Qy 1038 ---------- 1038
Db 7878 CTAGGTACTATTTAAGAATTTGGGCTGGGTGGACGTGGTAGCTCATTCCTGTAATCCCAG 7937
Qy 1038 ---------- 1038
Db 7938 CACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGTTCGAAACCAGCCTGGC 7997
Qy 1038 ---------- 1038
Db 7998 CAACATGGTGAAACCCTGTCTTTACTAAAAATACAAAAAATTAGCCAGGCGTGGTGGCAC 8057
Qy 1038 ---------- 1038
Db 8058 ATGCCAGTAATCCCAGCTACTTTGGAGGCTGAGGCAGAATTGCTTGAACCTGGGAGGCGA 8117
Qy 1038 ---------- 1038
Db 8118 AGGTTGCAGTGAGCTGAGATCGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACT 8177
Qy 1038 ---------- 1038
Db 8178 CTCCGTCTCAAAAAAAAAAAAAAAAAAGAATTTGGGCTGGGCACAGTGGCTCATGCCTGT 8237
Qy 1038 ---------- 1038
Db 8238 AATTGGGATGATGCTGGGGCATTTTGGGAGGCCAAGGCAGGCGGATCCCCTGAAGTCAGG 8297
Qy 1038 ---------- 1038
Db 8298 AGTTCAAGACCAGCCTGGCCAACATTGCAAAACCCCGTCTCTACTGAAAATACAAAAATT 8357
Qy 1038 ---------- 1038
Db 8358 AGCTGGGCGTGGTGGCTCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA 8417
Qy 1038 ---------- 1038
Db 8418 TTACTTGAACCCAGGAGGCGGAGGTTACAGTGAGCTGAGATCACATCACTGTACTCCAGC 8477
Qy 1038 ---------- 1038
Db 8478 CTGGGCAAAAGAGCAAGATTCAATCTTCAAAAAAAGAATTTGGAAAATAAAAATAAAAAG 8537
Qy 1038 ---------- 1038
Db 8538 AATACGGGATATAATAGCAATACAGTTTTTTACCTCCAAGGAACTTATATTCTAGGGATA 8597
Qy 1038 ---------- 1038
Db 8598 GAGATAGACAATAAGGGCTGGGTGAGGTGGCTTACGCCTGTAATCCCAGCACTTTGGGAA 8657
Qy 1038 ---------- 1038
Db 8658 GCCGAGGTGGGCACATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCGACATGGTGA 8717
Qy 1038 ---------- 1038
Db 8718 AACCCCATCTCTACTAAAAATATGAAAATTAGCTGGGTGTGGGGGTGCATGCCTGTAATC 8777
Qy 1038 ---------- 1038
Db 8778 CCAGCTACTTGGAAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGGTGGAGGTTGCC 8837
Qy 1038 ---------- 1038
Db 8838 ATGAGCCGAGACCATGCCACTGCACTCCAGCCTGGGAGACCGAGCAAAACTCCATCTCAA 8897
Qy 1038 ---------- 1038
Db 8898 AAAAAGAAAAAAAAAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTG 8957
Qy 1038 ---------- 1038
Db 8958 CCCGGGCTTGTTTGTTTTAAGAGACAGGGTCTCACTCTGTCACCCAGGCTGTACCCTATT 9017
Qy 1038 ---------- 1038
Db 9018 TTCTACGTGTCTCTGTGTCTAAGCTCACCAAACCCATCCATACAGTGTTACCTAAAAGGA 9077
Qy 1038 ---------- 1038
Db 9078 CTCACGCATGCTCCCTGTACAGTTCCCATGAACTTAGTTCACCCAGCCTTTGGTGGGCCA 9137
Qy 1038 ---------- 1038
Db 9138 AGGTATCGTTGAGCTCTGAAGACAGATACAGCTCGGGACATGGCTGAGCTGGCCATGACT 9197
Qy 1039 ----------GlyPheLeuThrThrGlnGlyS 1046
Db 9198 GGCAGAGGAGCAGCTCCAGGACCACTCTGTTTTCCTAGGGCTTCCTGACCACCCAGGGCA 9257
Qy 1046 erArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGlyA 1066
Db 9258 GCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCCCCCGTGACCGATGGGG 9317
Qy 1066 laIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal- 1085
Db 9318 CCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCACTTTGACTTCATTGT-A 9376
Qy 1085 ---------- 1085
Db 9377 AGGTAGGGAGGGCTCGGGGCAGGGAGGCAGGGCTCAGGACAGGCCTGGGCTGACTCCCCC 9436
Qy 1086 ----------ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuL 1101
Db 9437 CACACCCTACCCCTAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTCC 9496
Qy 1101 euHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGlu---- 1119
Db 9497 TCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTGA 9556

```
Qy       1119 ------------------------------------------------------------ 1119

Db       9557 CCACACCCTCGGCACCATCCCTCTACTCCCAGCCCAAGGGACGGGGTAGGGAGAGGCAAG 9616

Qy       1119 ------------------------------------------------------------ 1119

Db       9617 GGAAGGGACAGAGCCCTGTGGCCCACAGACAGGTACCTCCCCAACAGGTGCCACCAGCTG 9676

Qy       1119 ------------------------------------------------------------ 1119

Db       9677 AAGGTGGCAGCCTCCTCCTTTCCCCAGACACCATGTTCCTGCCCCTCAGCCCTCCTGGCT 9736

Qy       1119 ------------------------------------------------------------ 1119

Db       9737 TCTTCATGGGACCCACCTTAGACTTTTAGGATCCAGAACAAGGTGCAGGGTTTGCCCCAG 9796

Qy       1119 ------------------------------------------------------------ 1119

Db       9797 GCCTCAACATCCTGTCGCCTGCCAGCTCTCATATCCTGCTGGAGACCAACAAGGGCCCCA 9856

Qy       1119 ------------------------------------------------------------ 1119

Db       9857 GCTTCCCAACAGTCATGGTAATCCCCAGCGAGATGCTAAAGGGGACGGGAGCCCCAGGGG 9916

Qy       1120 ----------------------------------ValIleGlnMetTyrLysGluSerP 1128
                                                  |||||||||||||||||||||||||

Db       9917 CCCGTGGGCTTACTGGGGCTGGTGTCTCCCCACAGGTGATACAGATGTACAAGGAAAGCC 9976

Qy       1128 roGluIleLeuSerProProAlaProGlnGlyGlyGlyLeuArgTrpGlyAlaSerSerS 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       9977 CAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGGCTTAGGTGGGGGGCATCCTCCT 10036

Qy       1148 erLeuProGlnSerPheAlaArgValThrThrSerMetThrValAlaIleHisProProP 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      10037 CCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATGACCGTGGCCATCCACCCACCCC 10096

Qy       1168 roLeuProGlyAlaTyrIleHisProAlaProAspGluProProTrpSerProAlaAlaT 1188
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |

Db      10097 CCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAGCCCCCTTGGTCCCCTGCTGTCA 10156

Qy       1188 hrSerSerGlyAsnLeuSerSerArgGlyProGlyProAlaThrGly 1203
              |||||||||||||||||||||||||||||||||||||||||||||||

Db      10157 CTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCAGCCACTGGG 10203
```

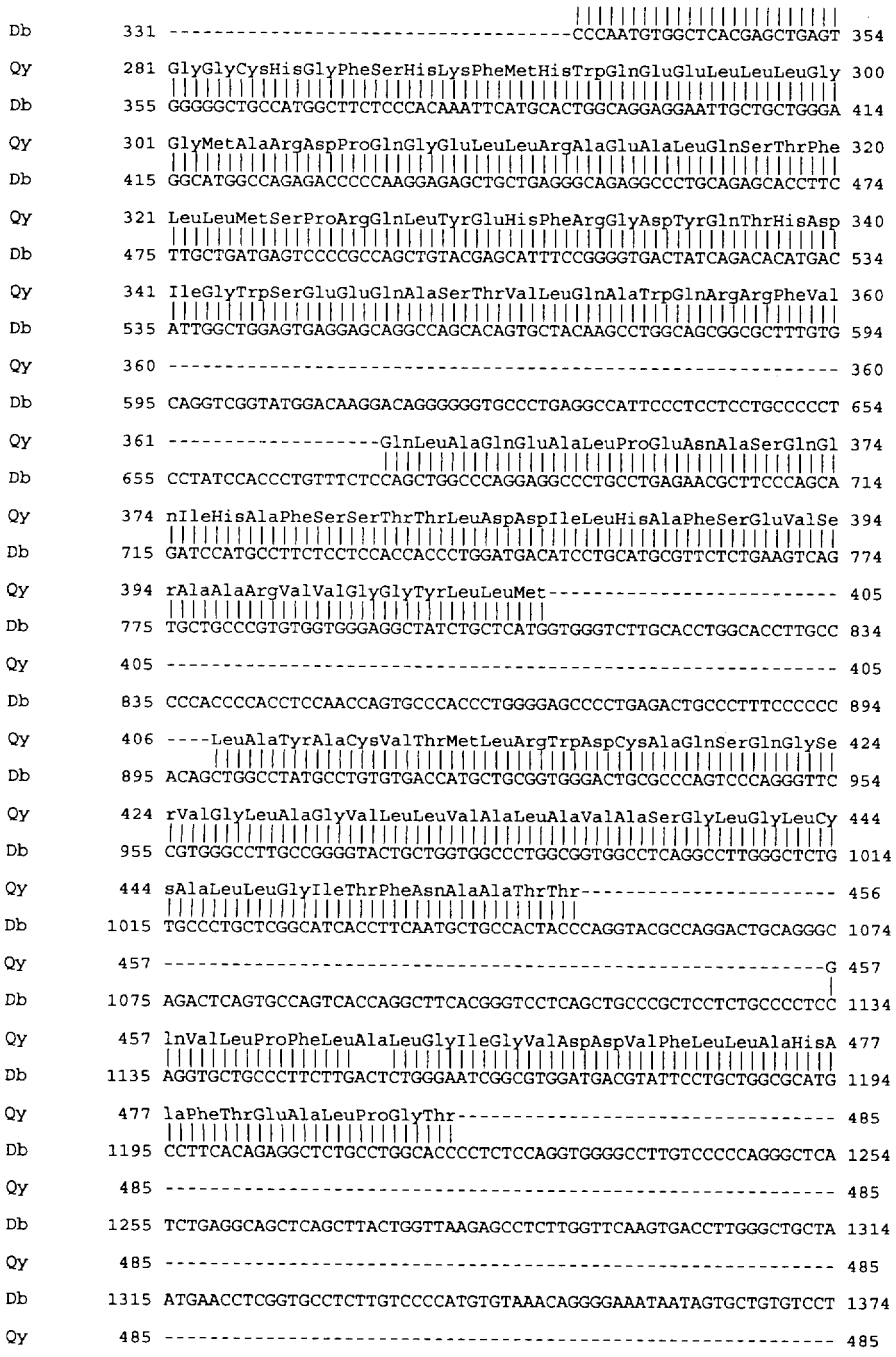
RESULT 7
AAZ31728
ID AAZ31728 standard; DNA; 4004 BP.
XX
AC AAZ31728;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human patched-2 coding sequence partial clone 3A.
XX
KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
KW cell proliferation; cell differentiation; testicular cancer; gut disease;
KW degenerative disorder; nervous system disorder; Parkinson's disease;
KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
KW therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9953058-A1.
XX
PD 21-OCT-1999.
XX
PF 02-APR-1999; 99WO-US007417.
XX
PR 15-APR-1998; 98US-00060939.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 1999-620428/53.
XX
PT New isolated human patched-2 gene, used to develop products for treating,
PT e.g. cancer and Alzheimer's disease.
XX
PS Example 1; Page 93-96; 124pp; English.
XX
CC This sequence is a partial clone of DNA encoding the human patched-2
CC (ptch-2) protein of the invention. The patched-2 polypeptides are
CC signalling molecules, specifically for signalling and mediator molecules
CC in the hedgehog (hh) cascade which are involved in cell proliferation and
CC differentiation. They can be used for the treatment of disorders which
CC are mediated at least in part by Hh, especially Dhh, e.g. testicular
CC cancer. They can also be used for treating degenerative disorders of the
CC nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
CC disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
CC stroke and drug addiction. Patched-2 agonists can be used to treat gut
CC diseases, bone diseases, skin diseases, diseases of the testis (including
CC infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
CC and osteoporosis. Antagonists or agonists of patched-2 may be used for
CC treating disorders or creating a desirable physiological condition
CC effected by blocking Hh signalling, especially Dhh signalling, e.g.
CC contraception or infertility treatment. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic animals
XX
SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

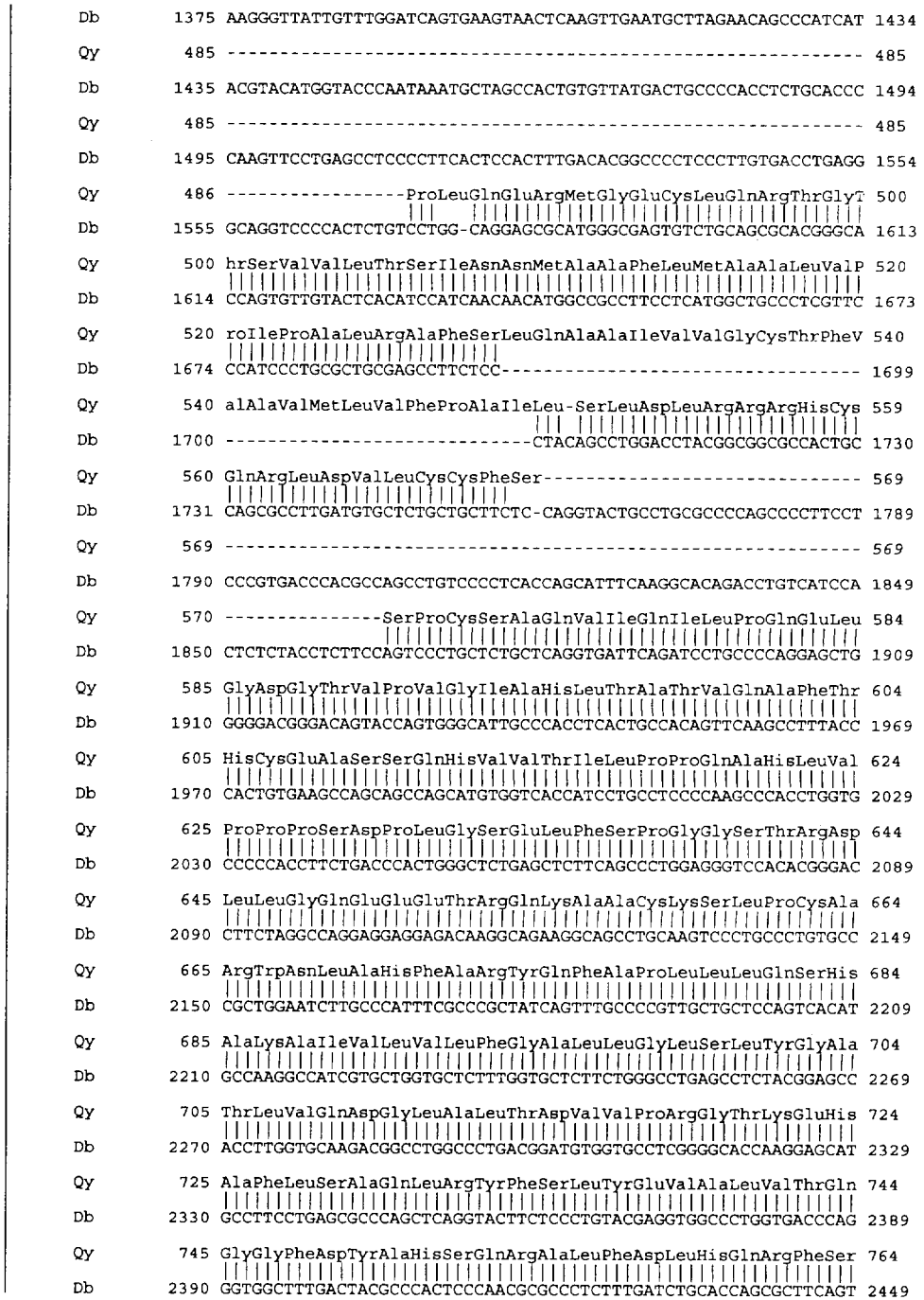
Alignment Scores:

Pred. No.:	2e-291	Length:	4004
Score:	3955.00	Matches:	847
Percent Similarity:	65.81%	Conservative:	2
Best Local Similarity:	65.66%	Mismatches:	10
Query Match:	63.06%	Indels:	434
DB:	2	Gaps:	10

US-09-990-046-2 (1-1203) x AAZ31728 (1-4004)

```
Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         11 CGGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 70

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         71 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 130

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 190

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        191 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        251 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 310

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||

Db        311 GGCTCCGCCTACCTGCCGCT---------------------------------------- 330

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240

Db        330 ------------------------------------------------------------ 330

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260

Db        330 ------------------------------------------------------------ 330

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
```


Db 331 ----------CCCAATGTGGCTCACGAGCTGAGT 354
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
Db 355 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 594
Qy 360 ---------- 360
Db 595 CAGGTCGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 654
Qy 361 ----------GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGl 374
Db 655 CCTATCCACCCTGTTTCTCCAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet---------- 405
Db 775 TGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGTGGGTCTTGCACCTGGCACCTTGCC 834
Qy 405 ---------- 405
Db 835 CCCACCCCACCTCCAACCAGTGCCCACCCTGGGGAGCCCCTGAGACTGCCCTTTCCCCCC 894
Qy 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 ----------G 457
Db 1075 AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTGCTGCCCTTCTTGACTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr---------- 485
Db 1195 CCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254
Qy 485 ---------- 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 ---------- 485
Db 1315 ATGAACCTCGGTGCCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGCTGTGTCCT 1374
Qy 485 ---------- 485


Db 1375 AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 ---------- 485
Db 1435 ACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 ---------- 485
Db 1495 CAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGAGG 1554
Qy 486 ----------ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCCACTCTGTCCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTTGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTC 1673
Qy 520 roIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC---------- 1699
Qy 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys 559
Db 1700 ----------CTACAGCCTGGACCTACGGCGGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCCTGCGCCCCAGCCCCTTCCT 1789
Qy 569 ---------- 569
Db 1790 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 1849
Qy 570 ----------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449

```
Qy       765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509

Qy       785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569

Qy       805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629

Qy       825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------------------- 837
            |||||||||||||||||||||||||||||||||||
Db      2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689

Qy       837 ---------------------------------------------------------- 837

Db      2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749

Qy       838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809

Qy       857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869

Qy       877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2870 AACTTCTACCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929

Qy       897 LeuArg------------------------------------------------------ 898
            ||||||
Db      2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989

Qy       898 ---------------------------------------------------------- 898

Db      2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049

Qy       899 -------------------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
                               :::||||||||||||||||||||||||||||||||||||||
Db      3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109

Qy       912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169

Qy       932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229

Qy       952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289

Qy       972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349

Qy       992 e---------------------------------------------------------- 992
            |
Db      3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

Qy       993 ----------------------------------------ValLeuValLeuAlaMetM 999
                                                    ||||||||||||||||||
Db      3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy       999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529
```

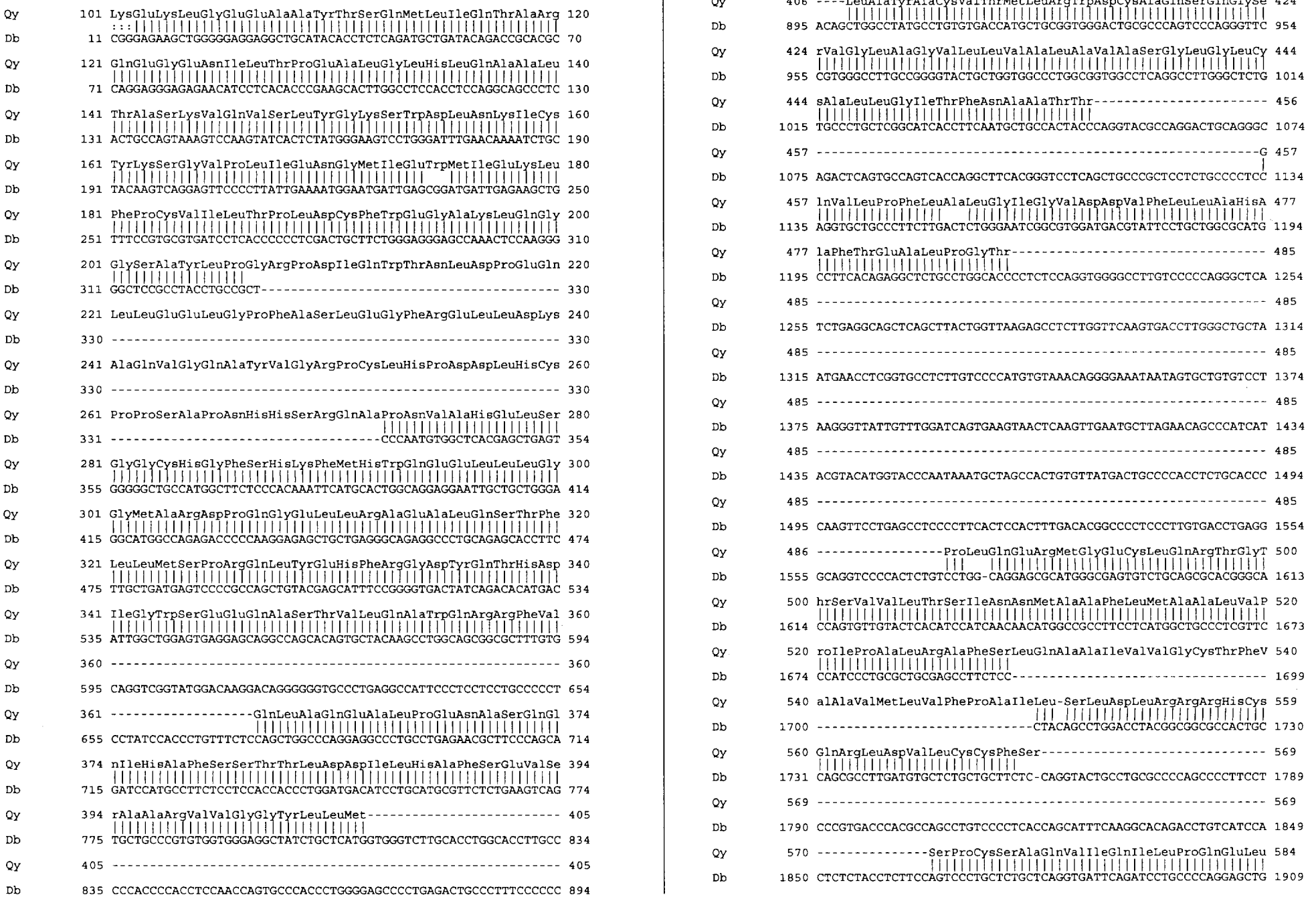
```
Qy      1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy      1039 lyPheLeuThrThrGlnGly 1045
                    |||   |||
Db      3590 TGAGCACGGGCACCCCGGGG 3609
```

RESULT 8
AAD31580
ID AAD31580 standard; cDNA; 4004 BP.
XX
AC AAD31580;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human patched-2 (Ptch-2) cDNA clone 3A.
XX
KW Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW cytostatic; testicular cancer; hedgehog protein signalling; clone 3A; ss.
XX
OS Homo sapiens.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT primer_bind 30. .50
FT /*tag= a
FT /bound_moiety= "RACE 6 PCR primer"
FT primer_bind complement(184. .204)
FT /*tag= b
FT /bound_moiety= "RACE 5 PCR primer"
XX
PN US6348575-B1.
XX
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081884P.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage F, Carpenter DA;
XX
DR WPI; 2002-215260/27.
XX
PT Native human patched-2 polypeptide for treating disorders caused by
PT Hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 10; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to Hedgehog, especially
CC Desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC Hedgehog protein signalling. The present sequence is human patched-2
CC (Ptch-2) cDNA clone 3A
XX
SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2e-291	Length:	4004
Score:	3955.00	Matches:	847
Percent Similarity:	65.81%	Conservative:	2
Best Local Similarity:	65.66%	Mismatches:	10
Query Match:	63.06%	Indels:	434
DB:	6	Gaps:	10

US-09-990-046-2 (1-1203) x AAD31580 (1-4004)



```
Qy       585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db      1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969

Qy       605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db      1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029

Qy       625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db      2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089

Qy       645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db      2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149

Qy       665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db      2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209

Qy       685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db      2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269

Qy       705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db      2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329

Qy       725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db      2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389

Qy       745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db      2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449

Qy       765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db      2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509

Qy       785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db      2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569

Qy       805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db      2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629

Qy       825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------------------- 837
Db      2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689

Qy       837 ------------------------------------------------------------ 837
Db      2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749

Qy       838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
Db      2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809

Qy       857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
Db      2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869

Qy       877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
Db      2870 AACTTCTACCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929

Qy       897 LeuArg-------------------------------------------------------- 898
Db      2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989

Qy       898 ------------------------------------------------------------ 898
```

```
Db      2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049

Qy       899 -------------------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db      3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109

Qy       912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db      3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169

Qy       932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db      3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229

Qy       952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db      3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289

Qy       972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
Db      3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349

Qy       992 e------------------------------------------------------------ 992
Db      3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

Qy       993 ----------------------------------------ValLeuValLeuAlaMetM 999
Db      3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy       999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
Db      3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529

Qy      1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
Db      3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy      1039 lyPheLeuThrThrGlnGly 1045
Db      3590 TGAGCACGGGCACCCCGGGG 3609
```

RESULT 9
ABX15923
ID ABX15923 standard; cDNA; 4004 BP.
XX
AC ABX15923;
XX
DT 02-APR-2003 (first entry)
XX
DE Human partial cDNA for patched-2 from brain.
XX
KW Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX
OS Homo sapiens.
XX
PN US2002156245-A1.
XX
PD 24-OCT-2002.
XX
PF 20-NOV-2001; 2001US-00990046.
XX
PR 15-APR-1998; 98US-0081884P.
PR 15-APR-1999; 99US-00293505.
XX
PA (GETH) GENENTECH INC.

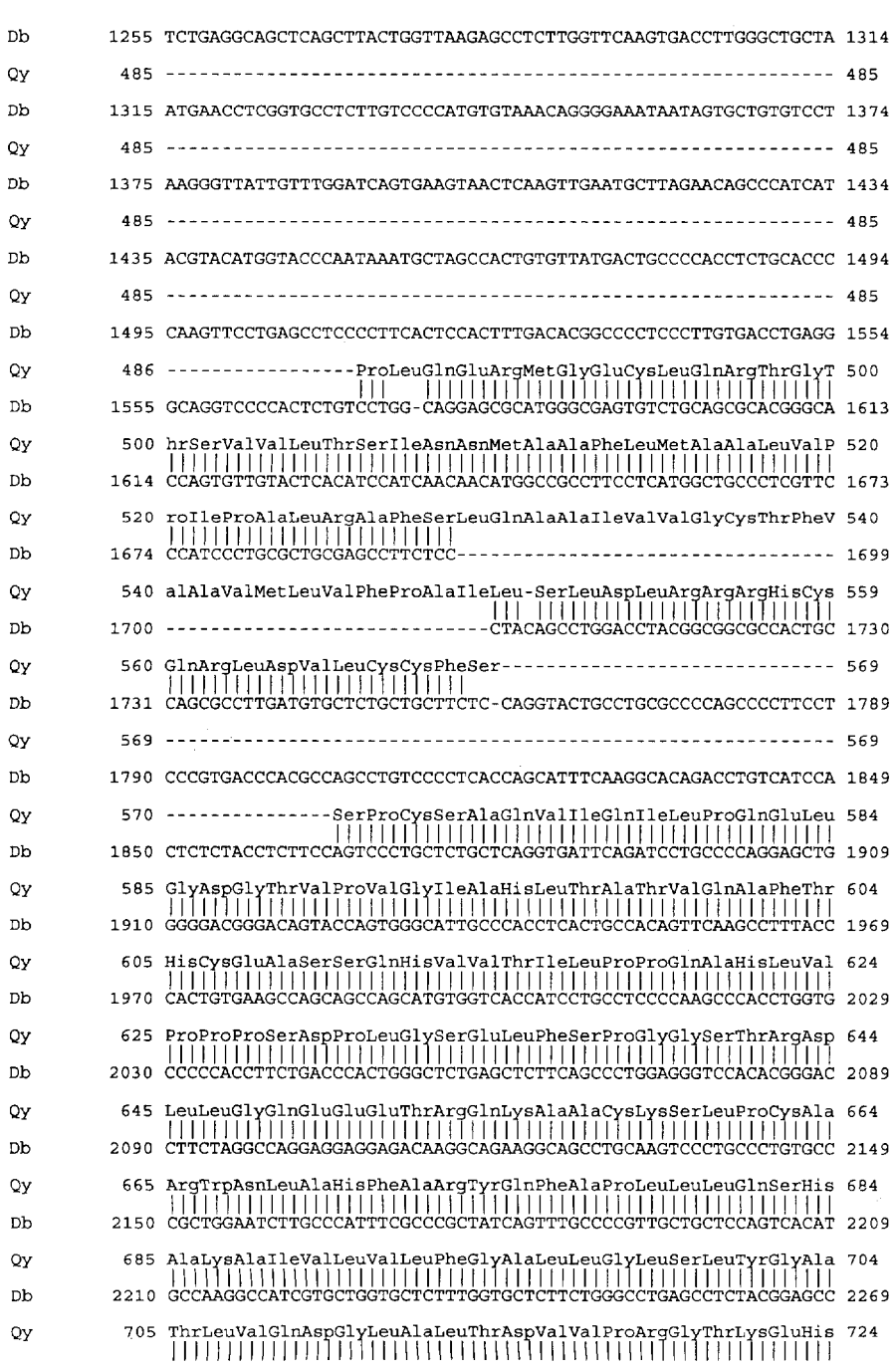
XX
PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 2003-182650/18.
XX
PT New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT e.g., testicular cancer.
XX
PS Example 1; Fig 10; 85pp; English.
XX
CC The invention relates to a new isolated nucleic acid encoding a
CC polypeptide having patched-2 biological activity, comprises DNA having at
CC least 95% sequence identity with a DNA molecule or its complement
CC encoding: (a) a human patched-2 polypeptide comprising the sequence
CC ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC Deposit No. 209778 designation). Also included are a vector comprising
CC the nucleic acid, a host cell transformed with the vector, a process for
CC producing patched-2 polypeptides, an isolated native sequence of human
CC patched-2 polypeptide, a chimaeric molecule comprising the vertebrate
CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC patched-2 that stimulates or enhances the normal functioning of patched-2
CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC and diagnosing to determine whether a particular disorder is modulated
CC The nucleic acid is useful for manufacturing a medicament for diagnosing
CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC Patched-2 may also be used to develop male contraceptives. The gene for
CC Patched-2 is located on human chromosome 1p33-34. The present sequence is
CC a Human partial cDNA for patched-2 from brain
XX
SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2e-291	Length:	4004
Score:	3955.00	Matches:	847
Percent Similarity:	65.81%	Conservative:	2
Best Local Similarity:	65.66%	Mismatches:	10
Query Match:	63.06%	Indels:	434
DB:	8	Gaps:	10

US-09-990-046-2 (1-1203) x ABX15923 (1-4004)

```
Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 CGGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 70

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 130

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 190

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 310

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||
Db        311 GGCTCCGCCTACCTGCCGCT---------------------------------------- 330

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db        330 ---------------------------------------------------------- 330

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db        330 ---------------------------------------------------------- 330

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
                                                  ||||||||||||||||||||||||
Db        331 ----------------------------------CCCAATGTGGCTCACGAGCTGAGT 354

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 594

Qy        360 ---------------------------------------------------------- 360
Db        595 CAGGTCGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 654

Qy        361 -------------------GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGl 374
                                  ||||||||||||||||||||||||||||||||||||||||
Db        655 CCTATCCACCCTGTTTCTCCAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCA 714

Qy        374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 GATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAG 774

Qy        394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet-------------------------- 405
              ||||||||||||||||||||||||||||||||
Db        775 TGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGTGGGTCTTGCACCTGGCACCTTGCC 834

Qy        405 ---------------------------------------------------------- 405
Db        835 CCCACCCCACCTCCAACCAGTGCCCACCCTGGGGAGCCCCTGAGACTGCCCTTTCCCCCC 894

Qy        406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 ACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTTC 954

Qy        424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 CGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCTG 1014

Qy        444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------------------- 456
              ||||||||||||||||||||||||||||||||||||
Db       1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGGC 1074

Qy        457 ----------------------------------------------------------G 457
                                                                         |
Db       1075 AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTCC 1134

Qy        457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1135 AGGTGCTGCCCTTCTTGACTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATG 1194

Qy        477 laPheThrGluAlaLeuProGlyThr---------------------------------- 485
              ||||||||||||||||||||||||
Db       1195 CCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254

Qy        485 ---------------------------------------------------------- 485
```


Db 1255 TCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 ---------- 485
Db 1315 ATGAACCTCGGTGCCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGCTGTGTCCT 1374
Qy 485 ---------- 485
Db 1375 AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 ---------- 485
Db 1435 ACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 ---------- 485
Db 1495 CAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGAGG 1554
Qy 486 ----------ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCCACTCTGTCCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTTGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTC 1673
Qy 520 roIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC---------- 1699
Qy 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys 559
Db 1700 ----------CTACAGCCTGGACCTACGGCGGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCCTGCGCCCCAGCCCCTTCCT 1789
Qy 569 ---------- 569
Db 1790 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 1849
Qy 570 ----------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------- 837
Db 2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689
Qy 837 ---------- 837
Db 2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749
Qy 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
Db 2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809
Qy 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
Db 2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869
Qy 877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
Db 2870 AACTTCTACCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929
Qy 897 LeuArg---------- 898
Db 2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989
Qy 898 ---------- 898
Db 2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049
Qy 899 ----------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db 3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109
Qy 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db 3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169
Qy 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db 3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229
Qy 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db 3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289
Qy 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
Db 3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349
Qy 992 e---------- 992
Db 3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

```
Qy        993 ----------------------------------------ValLeuValLeuAlaMetM 999
                                                      ||||||||||||||||||
Db       3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy        999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529

Qy       1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy       1039 lyPheLeuThrThrGlnGly 1045
                 |||   |||
Db       3590 TGAGCACGGGCACCCCGGGG 3609

RESULT 10
AAZ31729
ID   AAZ31729 standard; DNA; 2082 BP.
XX
AC   AAZ31729;
XX
DT   19-JAN-2000  (first entry)
XX
DE   Human patched-2 coding sequence partial clone 16.1.
XX
KW   Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
KW   cell proliferation; cell differentiation; testicular cancer; gut disease;
KW   degenerative disorder; nervous system disorder; Parkinson's disease;
KW   memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
KW   Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
KW   infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9953058-A1.
XX
PD   21-OCT-1999.
XX
PF   02-APR-1999;   99WO-US007417.
XX
PR   15-APR-1998;   98US-00060939.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage FJ,  Carpenter DA;
XX
DR   WPI; 1999-620428/53.
XX
PT   New isolated human patched-2 gene, used to develop products for treating,
PT   e.g. cancer and Alzheimer's disease.
XX
PS   Example 1; Page 96-97; 124pp; English.
XX
CC   This sequence is a partial clone of DNA encoding the human patched-2
CC   (ptch-2) protein of the invention. The patched-2 polypeptides are
CC   signalling molecules, specifically for signalling and mediator molecules
CC   in the hedgehog (hh) cascade which are involved in cell proliferation and
CC   differentiation. They can be used for the treatment of disorders which
CC   are mediated at least in part by Hh, especially Dhh, e.g. testicular
CC   cancer. They can also be used for treating degenerative disorders of the
CC   nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
CC   disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
CC   stroke and drug addiction. Patched-2 agonists can be used to treat gut
CC   diseases, bone diseases, skin diseases, diseases of the testis (including
CC   infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
CC   and osteoporosis. Antagonists or agonists of patched-2 may be used for
CC   treating disorders or creating a desirable physiological condition
CC   effected by blocking Hh signalling, especially Dhh signalling, e.g.
CC   contraception or infertility treatment. The products can also be used for
CC   detection, diagnosis, drug screening and production of transgenic animals
XX
SQ   Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.82e-248      Length:          2082
Score:                    3387.00        Matches:         656
Percent Similarity:       96.33%         Conservative:    1
Best Local Similarity:    96.19%         Mismatches:      3
Query Match:              54.00%         Indels:          23
DB:                       2              Gaps:            2

US-09-990-046-2 (1-1203) x AAZ31729 (1-2082)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907
```

```
Qy       301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy       321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db      1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db      1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT---------------TTCGCCCCGGAATTC 1980

Qy       681 LeuGln 682
Db      1981 CTGCAG 1986
```

RESULT 11
AAD31581
ID AAD31581 standard; cDNA; 2082 BP.
XX
AC AAD31581;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human patched-2 (Ptch-2) cDNA clone 16.1.
XX
KW Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW cytostatic; testicular cancer; hedgehog protein signalling; clone 16.1;
KW ss.
XX
OS Homo sapiens.
XX
PN US6348575-B1.
XX
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081884P.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage F, Carpenter DA;
XX
DR WPI; 2002-215260/27.
XX
PT Native human patched-2 polypeptide for treating disorders caused by
PT Hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 11; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to Hedgehog, especially
CC Desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC Hedgehog protein signalling. The present sequence is human patched-2
CC (Ptch-2) cDNA clone 16.1
XX
SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.82e-248	Length:	2082
Score:	3387.00	Matches:	656
Percent Similarity:	96.33%	Conservative:	1
Best Local Similarity:	96.19%	Mismatches:	3
Query Match:	54.00%	Indels:	23
DB:	6	Gaps:	2

US-09-990-046-2 (1-1203) x AAD31581 (1-2082)

```
Qy         1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db         8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy        21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db        68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127
```

```
Qy        41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db       128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy        61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db       188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy        81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db       248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy       101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db       308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367

Qy       121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db       368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy       141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db       428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy       161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db       488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547

Qy       181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db       548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy       201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db       608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy       221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db       668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy       241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db       728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy       261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy       281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907

Qy       301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy       321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db      1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db      1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT--------------TTCGCCCCGGAATTC 1980

Qy       681 LeuGln 682
Db      1981 CTGCAG 1986
```

RESULT 12
ABX15924
ID ABX15924 standard; cDNA; 2082 BP.
XX
AC ABX15924;
XX
DT 02-APR-2003 (first entry)
XX
DE Human partial cDNA for patched-2 from testis.
XX
KW Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;

KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX
OS Homo sapiens.
XX
PN US2002156245-A1.
XX
PD 24-OCT-2002.
XX
PF 20-NOV-2001; 2001US-00990046.
XX
PR 15-APR-1998; 98US-0081884P.
PR 15-APR-1999; 99US-00293505.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 2003-182650/18.
XX
PT New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT e.g., testicular cancer.
XX
PS Example 1; Fig 11; 85pp; English.
XX
CC The invention relates to a new isolated nucleic acid encoding a
CC polypeptide having patched-2 biological activity, comprises DNA having at
CC least 95% sequence identity with a DNA molecule or its complement
CC encoding: (a) a human patched-2 polypeptide comprising the sequence
CC ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC Deposit No. 209778 designation). Also included are a vector comprising
CC the nucleic acid, a host cell transformed with the vector, a process for
CC producing patched-2 polypeptides, an isolated native sequence of human
CC patched-2 polypeptide, a chimaeric molecule comprising the vertebrate
CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC patched-2 that stimulates or enhances the normal functioning of patched-2
CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC and diagnosing to determine whether a particular disorder is modulated
CC The nucleic acid is useful for manufacturing a medicament for diagnosing
CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC Patched-2 may also be used to develop male contraceptives. The gene for
CC Patched-2 is located on human chromosome 1p33-34. The present sequence is
CC a Human partial cDNA for patched-2 from testis
XX
SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.82e-248	Length:	2082
Score:	3387.00	Matches:	656
Percent Similarity:	96.33%	Conservative:	1
Best Local Similarity:	96.19%	Mismatches:	3
Query Match:	54.00%	Indels:	23
DB:	8	Gaps:	2

US-09-990-046-2 (1-1203) x ABX15924 (1-2082)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207
```

```
Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||
Db       1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
                                              ||||||||||||||||||||||||||||||
Db       1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
              ||||||||||||||||||||||||||||||                ||||||||
Db       1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT--------------TTCGCCCCGGAATTC 1980

Qy        681 LeuGln 682
              ||||||
Db       1981 CTGCAG 1986
```

RESULT 13
AAT14220

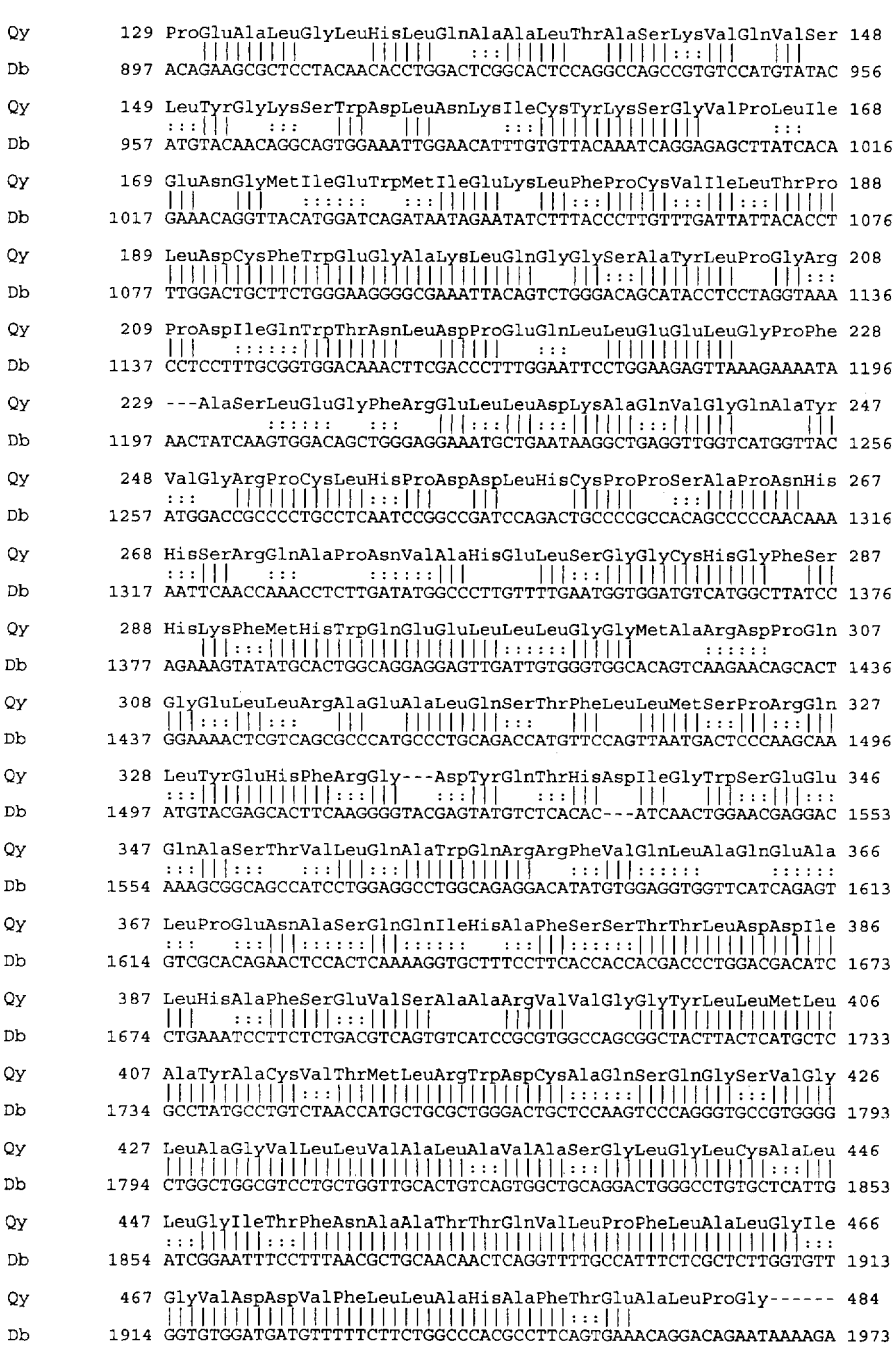
```
ID   AAT14220 standard; cDNA; 5288 BP.
XX
AC   AAT14220;
XX
DT   30-JUL-1996  (first entry)
XX
DE   Human patched gene.
XX
KW   Patched gene; ptc gene; embryo development; cellular regulation;
KW   signal transduction; ligand; antibody; hedgehog protein; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             384. .1427
FT                   /*tag=  a
XX
PN   WO9611260-A1.
XX
PD   18-APR-1996.
XX
PF   06-OCT-1995;   95WO-US013233.
XX
PR   07-OCT-1994;   94US-00319745.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Scott MP,  Goodrich LV,  Johnson RL;
XX
DR   WPI; 1996-209842/21.
DR   P-PSDB; AAR75375.
XX
PT   DNA encoding patched protein other than Drosophila patched protein - used
PT   to produce antibodies which detect or inhibit patched protein ligand
PT   signal transduction in cells.
XX
PS   Example; Page 53-56; 70pp; English.
XX
CC   A cDNA clone (AAT14220) coding for the human patched protein (PTC)
CC   (AAR75375) was obtd. by screening a human lung cDNA library with a 1 kb
CC   portion of the mouse ptc gene (see also AAT14218) and examination of
CC   isolated clones. The human ptc gene has about 89% identity to the mouse
CC   ptc gene. The 5' and 3' untranslated sequences are highly similar to
CC   mouse ptc, suggesting conservation of regulatory sequences. The human ptc
CC   gene can be used for prodn. of large amounts of recombinant PTC, as a
CC   probe e.g. to detect gene mutations, in gene therapy, to study embryo
CC   development, to produce transgenic animal models, etc
XX
SQ   Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	5.29e-245	Length:	5288
Score:	3349.00	Matches:	662
Percent Similarity:	70.02%	Conservative:	200
Best Local Similarity:	53.78%	Mismatches:	298
Query Match:	53.40%	Indels:	71
DB:	2	Gaps:	16

US-09-990-046-2 (1-1203) x AAT14220 (1-5288)

```
Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
              |||||||||          |||      |||      ||||||      |||
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
                   ||||||||||||||||||||||   ||||||   |||||||||   ||||||
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
              |||   ||||||::::::|||||||||   |||   :::|||||||||   |||||||||
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
                 |||:::||||||:::   |||   :::|||||||||:::|||:::||||||||||||
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
              ||||||   |||||||||:::|||||||:::||||||::::::|||:::||||||||||||
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
                 :::      |||::::::|||||||||   ::::::||||||   |||:::||||||
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896
```


Qy 129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db 897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956
Qy 149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db 957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016
Qy 169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db 1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076
Qy 189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db 1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136
Qy 209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db 1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196
Qy 229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db 1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256
Qy 248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316
Qy 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376
Qy 288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436
Qy 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496
Qy 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553
Qy 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613
Qy 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673
Qy 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733
Qy 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844

```
Db       3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104

Qy        845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864

Db       3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164

Qy        865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884

Db       3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224

Qy        885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903

Db       3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284

Qy        904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923

Db       3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344

Qy        924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943

Db       3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404

Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963

Db       3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464

Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983

Db       3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524

Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003

Db       3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584

Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023

Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043

Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063

Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083

Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103

Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123

Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys-----------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139

Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG---------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159

Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167

Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180

Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190

Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

RESULT 14
AAV64093
ID AAV64093 standard; cDNA; 5288 BP.
XX
AC AAV64093;
XX
DT 26-JAN-1999 (first entry)
XX
DE Human patched gene.
XX
KW Human; patched gene; diagnosis; treatment; developmental disorder;
KW cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
KW sperm production; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   384. .4727
FT   /*tag= a
XX
PN US5837538-A.
XX
PD 17-NOV-1998.
XX
PF 06-OCT-1995; 95US-00540406.
XX
PR 07-OCT-1994; 94US-00319745.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
DR WPI; 1999-023461/02.
DR P-PSDB; AAW72969.
XX
PT Nucleic acid encoding vertebrate patched protein and related
PT transformants - used to express poly:peptide(s), useful for diagnosis and
PT treatment of developmental disorders or cancer, and in healing of injured
PT tissue.
XX
PS Claim 1; Col 59-64; 38pp; English.
XX
CC The present sequence represents the human patched (ptc) gene. Cells
CC containing and expressing the ptc gene are used for the recombinant
CC production of the protein. These in turn are useful: (i) for generating
CC antibodies (Ab); and (ii) to screen for specific-binding ligands
CC (potential therapeutic agonists and antagonists). The ptc gene, or its
CC fragments, are used to isolate related sequences from other mammals; to
CC identify mutations (particularly those associated with genetic diseases
CC such as spina bifida and other developmental disorders); to monitor
CC expression levels in testis (to determine relationship with sperm
CC production) and to isolate 5'-non-coding sequences (used to study
CC embryonic development and to provide regulated expression of proteins).
CC The complete gene can be used in gene therapy, including expression of
CC antisense molecules, and to generate transgenic animals for studies of
CC embryonic development. Ab are used diagnostically to determine the ptc
CC protein on cell surfaces and as competitive inhibitors of signal
CC transduction through the ptc ligand. Cells that have been engineered to
CC express the ptc protein can be used to promote regrowth and healing of
CC damaged tissue (e.g. growth of new teeth) and regulation of the ptc
CC protein expression may be useful in cancer treatment (it may control the
CC Wnt-1 oncogene)
XX
SQ Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.29e-245 Length: 5288

Score:	3349.00	Matches:	662
Percent Similarity:	70.02%	Conservative:	200
Best Local Similarity:	53.78%	Mismatches:	298
Query Match:	53.40%	Indels:	71
DB:	2	Gaps:	16

US-09-990-046-2 (1-1203) x AAV64093 (1-5288)

```
Qy        12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db       540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy        31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db       597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy        49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db       657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy        69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db       717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy        89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db       777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy       109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db       837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy       129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db       897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy       149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db       957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy       169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrPro 188
Db      1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy       189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db      1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy       209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db      1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy       229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db      1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy       248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db      1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy       268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db      1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy       288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db      1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy       308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db      1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy       328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
```

```
Db      1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy       347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db      1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy       367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db      1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy       387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db      1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy       407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db      1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy       427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db      1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy       447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db      1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy       467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db      1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973

Qy       485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db      1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033

Qy       505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db      2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093

Qy       525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db      2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153

Qy       545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db      2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213

Qy       565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db      2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273

Qy       585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db      2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333

Qy       596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db      2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393

Qy       609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db      2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453

Qy       628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db      2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513

Qy       645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db      2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567

Qy       665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
```

```
Db       2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy        685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db       2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy        705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db       2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy        725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db       2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy        745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db       2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy        765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db       2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy        785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db       2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy        805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db       2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy        825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db       3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy        845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db       3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy        865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db       3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy        885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db       3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy        904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db       3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy        924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db       3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db       3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464
Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db       3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524
Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db       3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584
Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644
Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764
Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824
Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884
Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944
Qy       1123 tTyrLys----------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG---------- 3993
Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022
Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082
Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142
Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

RESULT 15
AAF32185
ID AAF32185 standard; DNA; 5288 BP.
XX
AC AAF32185;
XX
DT 12-APR-2001 (first entry)
XX
DE Human patched gene.
XX
KW Human; patched; PTC; segment polarity; limb patterning; development;
KW hedgehog; antibody; mouse; ds.
XX
OS Homo sapiens.
XX
PN US6172200-B1.
XX
PD 09-JAN-2001.
XX
PF 20-OCT-1997; 97US-00954668.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
XX
PA (STRD) UNIV LELAND S STANFORD.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
DR WPI; 2001-136884/14.
DR P-PSDB; AAB67163.
XX
PT Novel monoclonal antibody useful in diagnostic assays for detection of
PT presence of protein on surface of cells specifically binds to naturally
PT occurring patched protein, other than Drosophila patched protein.
XX
PS Disclosure; Col 57-62; 39pp; English.

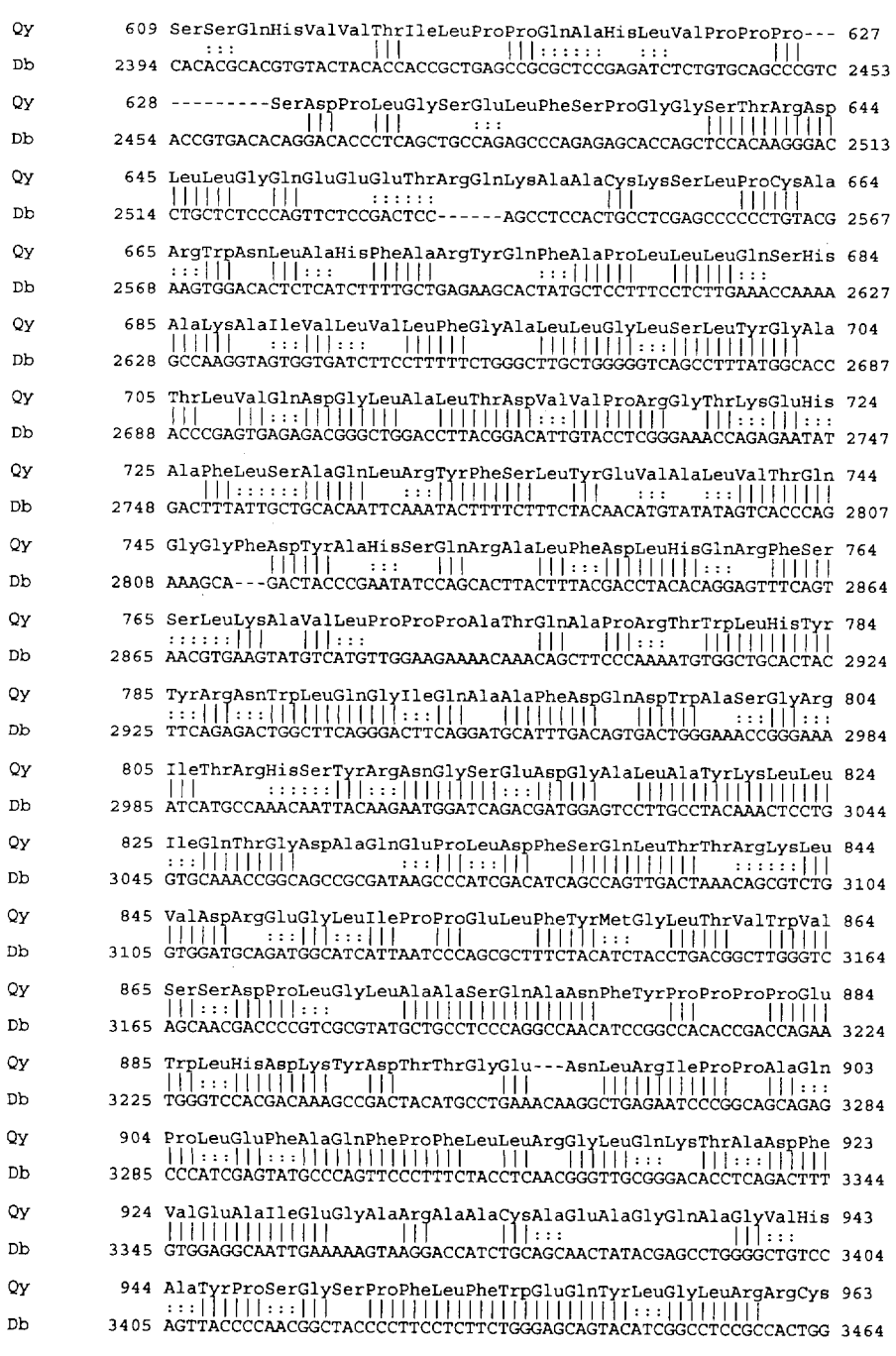
XX
CC The present invention provides a monoclonal antibody which specifically
CC binds to a patched protein (PTC) other than that from Drosophila. Also
CC given are the protein and coding sequences of patched from the beetle,
CC mouse, butterfly, fruit fly, mosquito and human. Patched is a segment
CC polarity gene involved in limb patterning. The sequences can be used to
CC study development and to isolate the patched ligand, hedgehog. In
CC addition, antibodies can be used to detect the PTC protein on cell
CC surfaces or to inhibit the transduction of signal by the PTC ligand by
CC competing for its binding site
XX
SQ Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.29e-245	Length:	5288
Score:	3349.00	Matches:	662
Percent Similarity:	70.02%	Conservative:	200
Best Local Similarity:	53.78%	Mismatches:	298
Query Match:	53.40%	Indels:	71
DB:	5	Gaps:	16

US-09-990-046-2 (1-1203) x AAF32185 (1-5288)

```
Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267

Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db       1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy        427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db       1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy        447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db       1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy        467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db       1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973

Qy        485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db       1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033

Qy        505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db       2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093

Qy        525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db       2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153

Qy        545 ValProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db       2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213

Qy        565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db       2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273

Qy        585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db       2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333

Qy        596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db       2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
```



Search completed: November 22, 2004, 08:25:16
Job time : 1032 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 22, 2004, 07:57:40 ; Search time 327 Seconds
(without alignments)
1302.800 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	1203	9	US-09-990-046-2	Sequence 2, Appli
2	6248	99.6	1203	9	US-09-909-280A-2	Sequence 2, Appli
3	5599	89.3	1182	9	US-09-990-046-7	Sequence 7, Appli
4	3348	53.4	1447	8	US-08-954-701A-19	Sequence 19, Appl
5	3348	53.4	1447	9	US-09-898-533-5	Sequence 5, Appli
6	3348	53.4	1447	10	US-09-754-032-19	Sequence 19, Appl
7	3348	53.4	1447	14	US-10-421-446-19	Sequence 19, Appl
8	3337	53.2	1434	8	US-08-954-701A-10	Sequence 10, Appl
9	3337	53.2	1434	10	US-09-754-032-10	Sequence 10, Appl
10	3337	53.2	1434	14	US-10-421-446-10	Sequence 10, Appl
11	3048	48.6	1296	14	US-10-302-279-60	Sequence 60, Appl
12	2235	35.6	1311	8	US-08-954-701A-4	Sequence 4, Appli
13	2235	35.6	1311	10	US-09-754-032-4	Sequence 4, Appli
14	2235	35.6	1311	14	US-10-421-446-4	Sequence 4, Appli
15	1992	31.8	1286	9	US-09-898-533-3	Sequence 3, Appli
16	1961.5	31.3	1299	8	US-08-954-771-48	Sequence 48, Appl
17	1961.5	31.3	1299	17	US-10-647-654-48	Sequence 48, Appl
18	1936.5	30.9	1285	8	US-08-954-701A-6	Sequence 6, Appli
19	1936.5	30.9	1285	10	US-09-754-032-6	Sequence 6, Appli
20	1936.5	30.9	1285	14	US-10-421-446-6	Sequence 6, Appli
21	1708.5	27.2	1405	14	US-10-369-493-5464	Sequence 5464, Ap
22	992	15.8	714	14	US-10-369-493-5410	Sequence 5410, Ap
23	640	10.2	1278	14	US-10-208-731-2	Sequence 2, Appli
24	640	10.2	1278	16	US-10-741-601-530	Sequence 530, App
25	602.5	9.6	1319	14	US-10-208-731-4	Sequence 4, Appli
26	600.5	9.6	1359	15	US-10-621-758A-44	Sequence 44, Appl
27	600.5	9.6	1359	16	US-10-663-208A-44	Sequence 44, Appl
28	600.5	9.6	1359	16	US-10-646-301A-44	Sequence 44, Appl
29	600.5	9.6	1359	16	US-10-736-769-44	Sequence 44, Appl
30	596	9.5	1331	15	US-10-621-758A-2	Sequence 2, Appli
31	596	9.5	1331	16	US-10-663-208A-2	Sequence 2, Appli
32	596	9.5	1331	16	US-10-646-301A-2	Sequence 2, Appli
33	596	9.5	1331	16	US-10-736-769-2	Sequence 2, Appli
34	590	9.4	1332	14	US-10-239-316-9	Sequence 9, Appli
35	584	9.3	1332	15	US-10-621-758A-4	Sequence 4, Appli
36	584	9.3	1332	16	US-10-663-208A-4	Sequence 4, Appli
37	584	9.3	1332	16	US-10-646-301A-4	Sequence 4, Appli
38	584	9.3	1332	16	US-10-736-769-4	Sequence 4, Appli
39	557.5	8.9	1333	15	US-10-621-758A-12	Sequence 12, Appl
40	557.5	8.9	1333	16	US-10-663-208A-12	Sequence 12, Appl
41	557.5	8.9	1333	16	US-10-646-301A-12	Sequence 12, Appl
42	557.5	8.9	1333	16	US-10-736-769-12	Sequence 12, Appl
43	444	7.1	933	15	US-10-415-934-3	Sequence 3, Appli
44	434	6.9	1061	15	US-10-415-934-9	Sequence 9, Appli
45	413.5	6.6	954	14	US-10-060-756A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-990-046-2
; Sequence 2, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-046-2

Query Match 100.0%; Score 6272; DB 9; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
```

```
Qy       181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db       181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy       241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db       241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy       301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db       301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy       361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db       361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy       421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db       421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy       481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db       481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy       541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db       541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy       601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db       601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy       661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db       661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy       721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db       721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy       781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db       781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy       841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db       841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy       901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db       901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy       961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db       961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy      1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db      1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy      1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db      1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy      1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
Db      1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy      1201 ATG 1203
Db      1201 ATG 1203
```

```
RESULT 2
US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
;  APPLICANT: Bumcroft, David A.
;  TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
;  TITLE OF INVENTION:  THERETO
;  FILE REFERENCE: CIBT-P02-050
;  CURRENT APPLICATION NUMBER: US/09/909,280A
;  CURRENT FILING DATE:  2001-07-19
;  PRIOR APPLICATION NUMBER: US 09/207,857
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: US 60/067,940
;  PRIOR FILING DATE: 1997-12-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1203
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-909-280A-2

  Query Match             99.6%;  Score 6248;  DB 9;  Length 1203;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
Db         1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy        61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
Db        61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy       121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
Db       121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy       181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db       181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy       241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db       241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy       301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db       301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy       361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db       361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy       421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db       421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy       481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db       481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy       541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db       541 AVMLVFPAIFSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy       601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db       601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy       661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
```

```
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWMAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
Qy       1201 ATG 1203
Db       1201 ATG 1203
```

RESULT 3
US-09-990-046-7
; Sequence 7, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-990-046-7

Query Match 89.3%; Score 5599; DB 9; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60
Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120
Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180
Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240
Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300
Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360
Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420
Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db        421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480
Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db        481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540
Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db        541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600
Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db        601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660
Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db        661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720
Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db        781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840
Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db        841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db        901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960
Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db        961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db       1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080
Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db       1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140
Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
Db       1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181
```

RESULT 4
US-08-954-701A-19

```
; Sequence 19, Application US/08954701A
; Publication No. US20030032085A1
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,701A
;      FILING DATE:  20-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36709
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1447 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-954-701A-19

  Query Match             53.4%;  Score 3348;  DB 8;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 9e-267;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||    |  |   ||   |     |||||||| || ||| ||| ||:|||  | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:|  | :|  : | |  :|||||  :  | | :: :|| |:||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||||  |:||| |:|  ::|||  || : ||||      :: :  |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:|  |   || :||| :|  :   ::|   |:|||||  | |:|||||::||   ::
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:|||||:| :|  :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||||  :||:||  ||  |||||||||:|||||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
```

```
                ||||||||:||:|||||:|:||:|||||||||||||:||||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   |  |:|
Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||    |          |   :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                     : :|||  |  :  :    |   |:: :   |     | |  :       ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::      |    || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||    || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :|||   :|:| |||| ::||| :|:|  |  ||: || |||:||:  ||||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:||||| | ||: |:|||||| | |:  |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :|||||:|||||:|||||||||||||| |||  | :|  ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||  |||||||||| | :||:||:|:|||||||||   || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                   ::   |||          ||                             | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140
               |
Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 ----------------------------LRWG---------------ASSSLPQSFAR 1155
                                           |||                 ||:|
Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
               :||     |:|||:||||:||   :|
Db        1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 5
US-09-898-533-5
; Sequence 5, Application US/09898533
; Patent No. US20020106656A1
; GENERAL INFORMATION:
;  APPLICANT: Gemmill, Robert M.
;  APPLICANT:  Drabkin, Harry A.
;  TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
;  TITLE OF INVENTION:  PATCHED
```

```
;  FILE REFERENCE: 93445-00004
;  CURRENT APPLICATION NUMBER: US/09/898,533
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: US/09/268,140
;  PRIOR FILING DATE: 2000-03-12
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-898-533-5

  Query Match           53.4%;  Score 3348;  DB 9;  Length 1447;
  Best Local Similarity  49.9%;  Pred. No. 9e-267;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG---------------ASSSLPQSFAR 1155
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 6
US-09-754-032-19
; Sequence 19, Application US/09754032
; Publication No. US20030148388A1
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,032
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/540,406
;             FILING DATE: 06-OCT-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
```

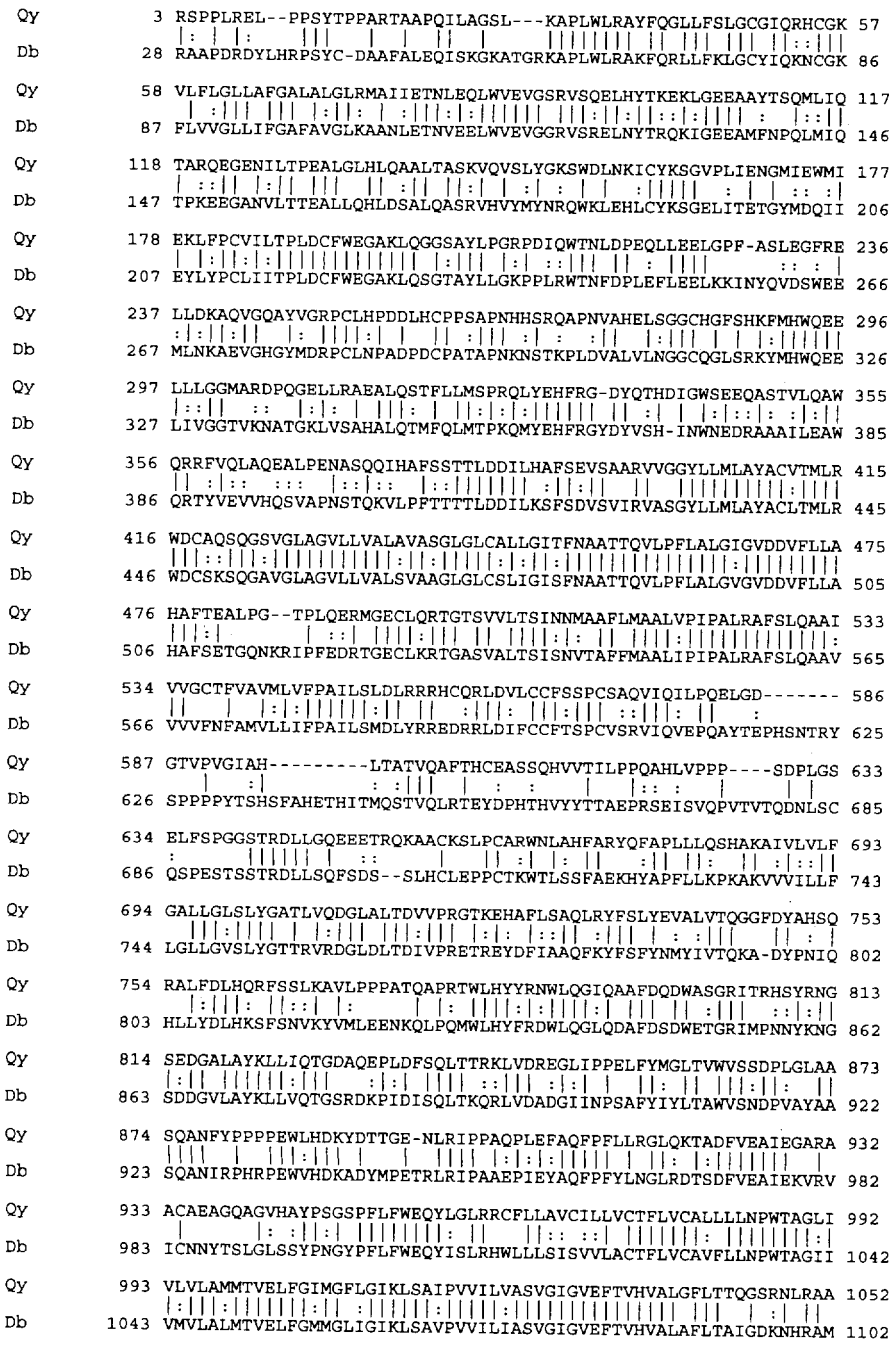
```
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1447 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-754-032-19

  Query Match             53.4%;  Score 3348;  DB 10;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 9e-267;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||    |  |  ||  |      |||||||| || ||| ||| ||::||| | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||| |:||| |:| ::||| || : |||| :: : |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:| |  || :||| :| :  ::|  |:||||| | |:|||||::||  ::
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:|:|||:| :| :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||||| :|:|:||  ||  ||||||||||:|||||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
               |||||||||:||:|||||:|:||:||||||||||||||:||||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:||||||||||||:||  |  |:|
Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |  :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   |:: :   |      | |  :      ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::     |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :///   :|:| |||| ::||| :|:| \  \|: || |||:||:  ||||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947
```

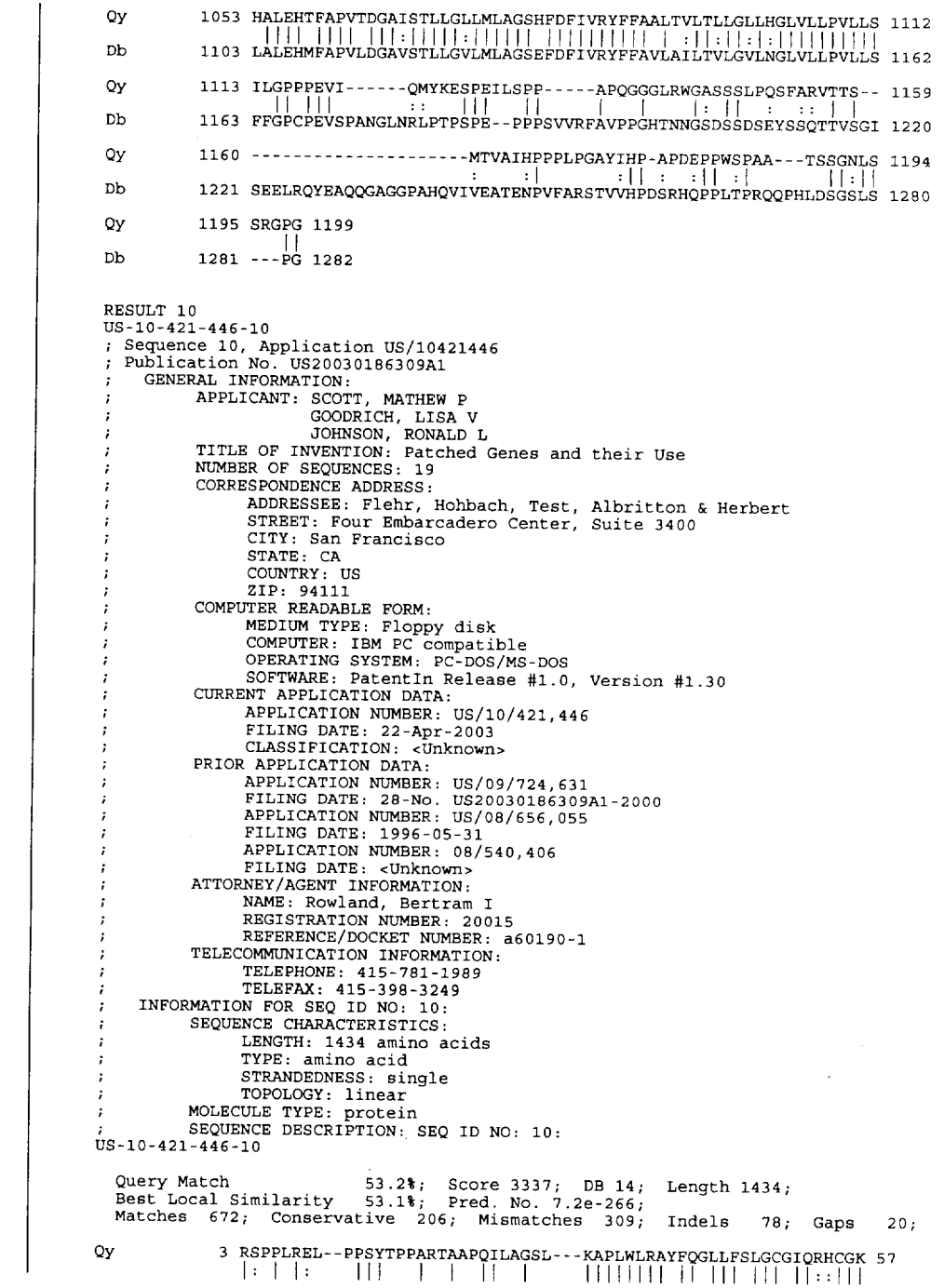
```
Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |  |:     |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :||||||:|||||:|||||||||||||||| ||| | :| ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                   ::   |||         ||                               | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140
               |
Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                 ||:|
Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
               :||     |:|||:||||:||   :|
Db        1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 7
US-10-421-446-19
; Sequence 19, Application US/10421446
; Publication No. US20030186309A1
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/421,446
;             FILING DATE: 22-Apr-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/724,631
;             FILING DATE: 28-No. US20030186309A1-2000
;             APPLICATION NUMBER: US/08/656,055
;             FILING DATE: 1996-05-31
;             APPLICATION NUMBER: 08/540,406
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
```

```
;            TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 1447 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-421-446-19

  Query Match           53.4%;  Score 3348;  DB 14;  Length 1447;
  Best Local Similarity  49.9%;  Pred. No. 9e-267;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
              |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
              |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
              |||||||||| |:||| |:| ::||| || : ||||       :: : |:|:||:||  |
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
              : ||||:| |  || :||| :| :  ::|  |:||||| | |:||||||::||  ::
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
              |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
              : :|::|:: :|::|||||| :||:|| ||  |||||||||:|||||::|||:||
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
              |||||||||:||:|||||:|:||:|||||||||||||||:||||||||||||:|
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
              | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   |  |:|
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
              :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |  :|
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   |:: :   |     | |  :          ||||
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
              || |  ::    |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
              | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:||: ||
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
              ::| |:      | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
              :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||

Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
              |:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |  |:    |:
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
              :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
              ||:|| :|||||:|||||:|||||||||||||||| |||  | :| ||  |||| ||||
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
              |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                  ::    |||       ||                             | ||
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
              |
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                ||:|
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
                  :||     |:|||:||||:||   :|
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 8
US-08-954-701A-10
; Sequence 10, Application US/08954701A
; Publication No. US20030032085A1
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,701A
;      FILING DATE:  20-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36709
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1434 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-954-701A-10

  Query Match             53.2%;  Score 3337;  DB 8;  Length 1434;
  Best Local Similarity   53.1%;  Pred. No. 7.2e-266;
  Matches  672;  Conservative  206;  Mismatches  309;  Indels   78;  Gaps   20;

Qy          3 RSPPLREL--PPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGK 57
              |: | |:    |||   |  |  ||  |     ||||||||  || ||| ||| ||::|||
Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86

Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
               | :||| ||| |:||: | :|||:|:|||||| |||:||:||::|:|||| :   |::||
Db         87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy        118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177
              | ::|| |:|| ||| || :|| ||:| | :| : | |  :|||||  : | | :: :|
Db        147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy        178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236
              | |:||:|:|||||||||||||| |:||| |:| ::||| || : ||||       :: : |
Db        207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy        237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296
              :|:||:||  |: ||||:| |  || :||| :| :  :||  |:||| | | |:||||||
Db        267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy        297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355
              |::||  ::  |:|: | |||: | ||:|:|:|||||| || :| | |:|::|: :|:||
Db        327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy        356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415
              || :|::  :::  |::|::  |:|||||||| :||:||  ||  |||||||||:|:|||
Db        386 QRTYVEVVHQSVAPNSTQKVLPFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445

Qy        416 WDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLA 475
              |||::|||:||||||||||:||:|||||:|:||:|||||||||||||:|||||||||
Db        446 WDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLA 505

Qy        476 HAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533
              |||:|       | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:
Db        506 HAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAV 565

Qy        534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------- 586
              ||    |  |:|:||||||:|| ||  :|||: |||:||| ::|||: ||   :
Db        566 VVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTEPHSNTRY 625

Qy        587 GTVPVGIAH---------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS 633
                |   :|         : :|||  |  :  :    |   |:: :   |      | |
Db        626 SPPPPYTSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDNLSC 685

Qy        634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLF 693
              :      ||||||  |  ::      |    || :| |: ||   :|| ||:  || :|::||
Db        686 QSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVILLF 743

Qy        694 GALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQ 753
              |||:|||| | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |
Db        744 LGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQ 802

Qy        754 RALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNG 813
              |:|||: ||::| |:      | |: ||||:|:||||:| ||| || :|||  ::|:||
Db        803 HLLYDLHKSFSNVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNNYKNG 862

Qy        814 SEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAA 873
              |:|| ||||||:|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||
Db        863 SDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAA 922

Qy        874 SQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA 932
              ||||  |  |||:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |
Db        923 SQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRV 982

Qy        933 ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLI 992
*
```

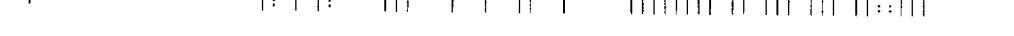
```
              |      |: :||:| |||||||: ||   ||:: ::| |||||||: ||||||||:|
Db        983 ICNNYTSLGLSSYPNGYPFLFWEQYISLRHWLLLSISVVLACTFLVCAVFLLNPWTAGII 1042

Qy        993 VLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAA 1052
              |:|||:|||||||:|| :||||||:|||||:|||||||||||||||| |||  | :| ||
Db       1043 VMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNHRAM 1102

Qy       1053 HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLS 1112
              |||| |||| |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||
Db       1103 LALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPVLLS 1162

Qy       1113 ILGPPPEVI------QMYKESPEILSPP-----APQGGGLRWGASSSLPQSFARVTTS-- 1159
                || |||       ::   |||   ||      |  |  |: ||  :  :: | |
Db       1163 FFGPCPEVSPANGLNRLPTPSPE--PPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220

Qy       1160 --------------------MTVAIHPPPLPGAYIHP-APDEPPWSPAA---TSSGNLS 1194
                                   :    :|       :|| :  :|| :|       ||:||
Db       1221 SEELRQYEAQQGAGGPAHQVIVEATENPVFARSTVVHPDSRHQPPLTPRQQPHLDSGSLS 1280

Qy       1195 SRGPG 1199
                ||
Db       1281 ---PG 1282


RESULT 9
US-09-754-032-10
; Sequence 10, Application US/09754032
; Publication No. US20030148388A1
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,032
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/540,406
;             FILING DATE: 06-OCT-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1434 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-754-032-10

  Query Match             53.2%;  Score 3337;  DB 10;  Length 1434;
  Best Local Similarity   53.1%;  Pred. No. 7.2e-266;
  Matches  672;  Conservative  206;  Mismatches  309;  Indels   78;  Gaps   20;
```





RESULT 10
US-10-421-446-10
; Sequence 10, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-421-446-10

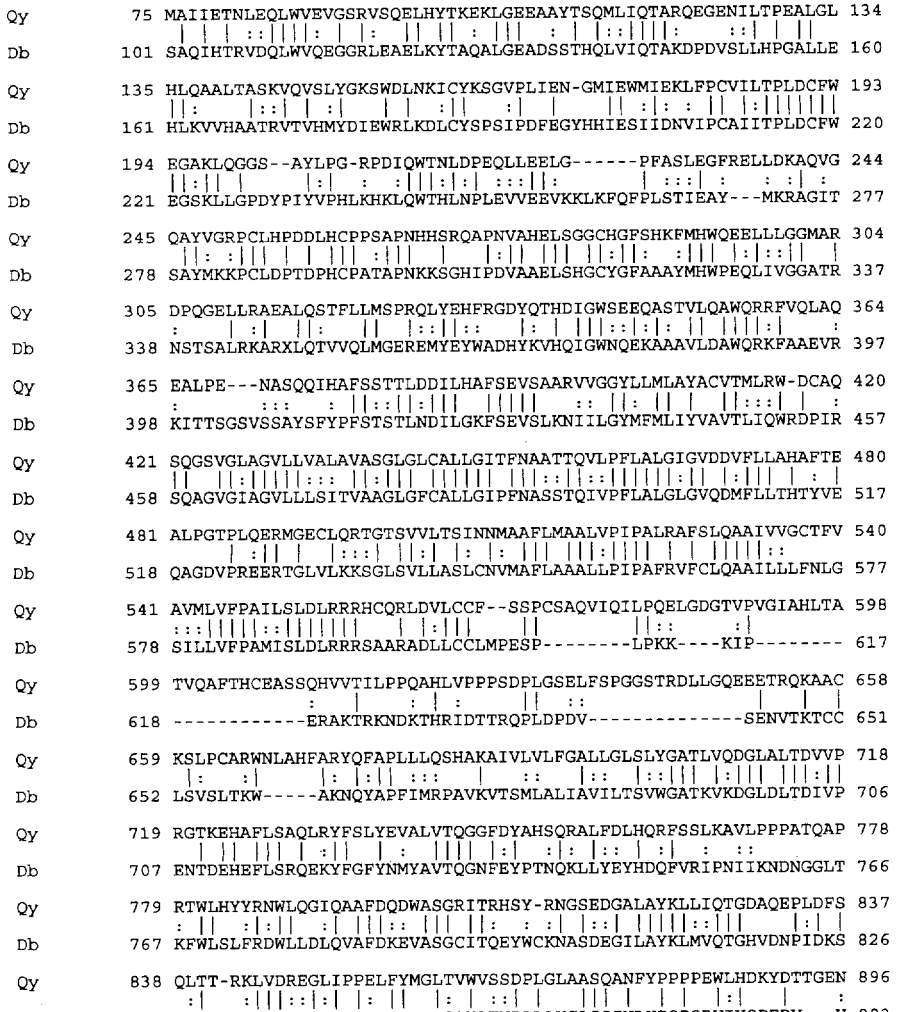
Query Match 53.2%; Score 3337; DB 14; Length 1434;
Best Local Similarity 53.1%; Pred. No. 7.2e-266;
Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;

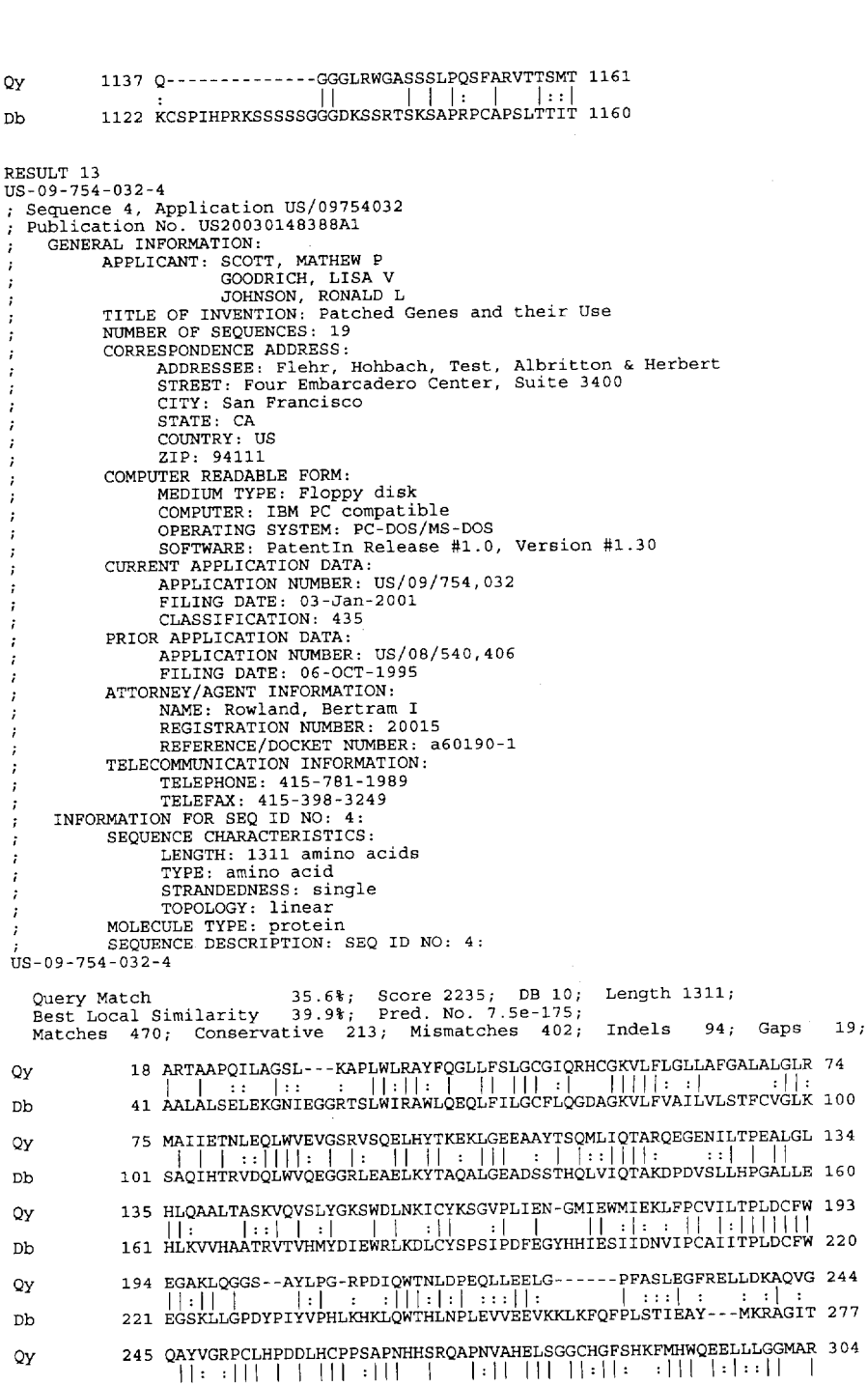


```
Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86

Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117

Db         87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy        118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177

Db        147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy        178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236

Db        207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy        237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296

Db        267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy        297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355

Db        327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy        356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415

Db        386 QRTYVEVVHQSVAPNSTQKVLPFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445

Qy        416 WDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLA 475

Db        446 WDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLA 505

Qy        476 HAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533

Db        506 HAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAV 565

Qy        534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------- 586

Db        566 VVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTEPHSNTRY 625

Qy        587 GTVPVGIAH---------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS 633

Db        626 SPPPPYTSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDNLSC 685

Qy        634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLF 693

Db        686 QSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVILLF 743

Qy        694 GALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQ 753

Db        744 LGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQ 802

Qy        754 RALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNG 813

Db        803 HLLYDLHKSFSNVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNNYKNG 862

Qy        814 SEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAA 873

Db        863 SDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAA 922

Qy        874 SQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA 932

Db        923 SQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRV 982

Qy        933 ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLI 992

Db        983 ICNNYTSLGLSSYPNGYPFLFWEQYISLRHWLLLSISVVLACTFLVCAVFLLNPWTAGII 1042

Qy        993 VLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAA 1052

Db       1043 VMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNHRAM 1102

Qy       1053 HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLS 1112

Db       1103 LALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPVLLS 1162

Qy       1113 ILGPPPEVI------QMYKESPEILSPP-----APQGGGLRWGASSSLPQSFARVTTS-- 1159

Db       1163 FFGPCPEVSPANGLNRLPTPSPE--PPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220

Qy       1160 --------------------MTVAIHPPPLPGAYIHP-APDEPPWSPAA---TSSGNLS 1194

Db       1221 SEELRQYEAQQGAGGPAHQVIVEATENPVFARSTVVHPDSRHQPPLTPRQQPHLDSGSLS 1280

Qy       1195 SRGPG 1199

Db       1281 ---PG 1282
```

RESULT 11
US-10-302-279-60
; Sequence 60, Application US/10302279
; Publication No. US20030171566A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael Carlton
; Hahn, Heidi Eve
; Wicking, Carol
; Christiansen, Jeffrey
; Zaphiropoulos, Peter G.
; Gailani, Mae R.
; Shanley, Susan Mary
; Chidambaram, Abirami
; Vorechovsky, Igor
; Holmberg-Lindstrom, Erika
; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/302,279
; FILING DATE: 22-No. US20030171566A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/857,636
; FILING DATE: 16-MAY-1997
; APPLICATION NUMBER: US 60/017,906
; FILING DATE: 17-MAY-1996
; APPLICATION NUMBER: AU PO0011
; FILING DATE: 21-MAY-1996
; APPLICATION NUMBER: AU PO0363
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 60/019,765
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35, 551
; REFERENCE/DOCKET NUMBER: 015280-278200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

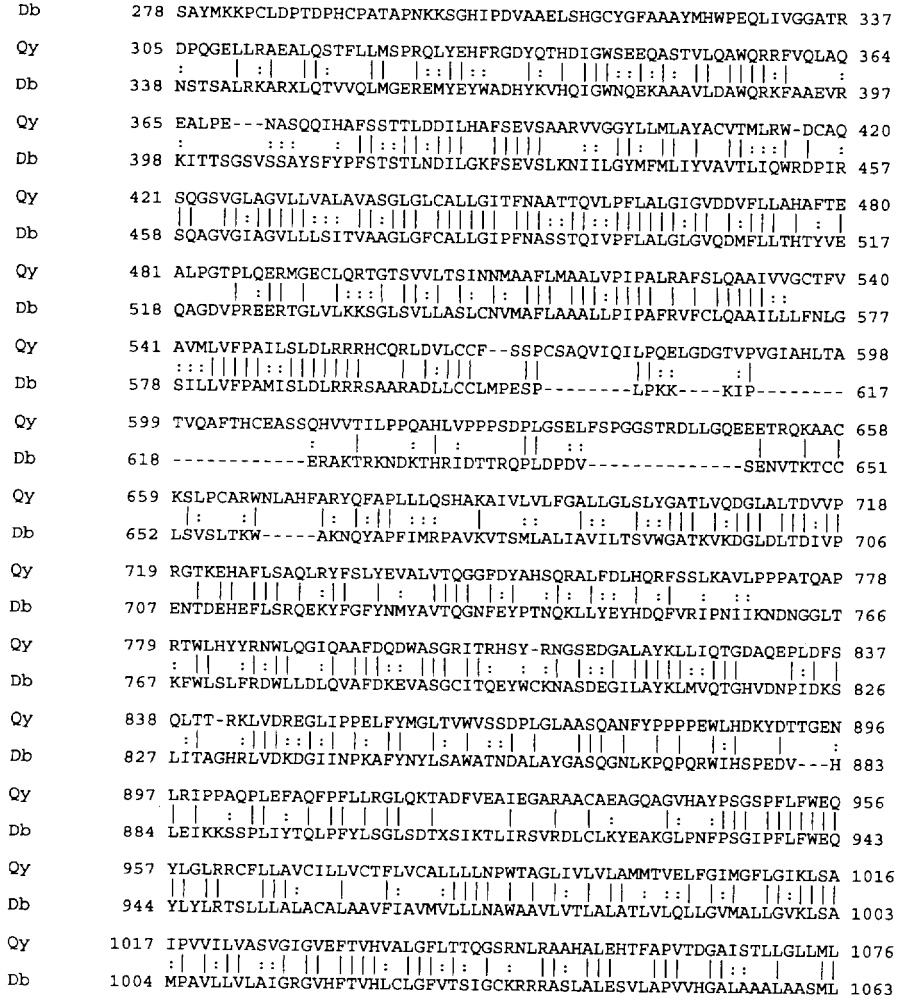
```
;             NAME/KEY:  Protein
;             LOCATION:  1..1296
;             OTHER INFORMATION:  /note= "amino acids encoded by human
;             nevoid basal cell carcinoma syndrome
;             (NBCCS) (PATCHED (PTC)) cDNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-302-279-60

  Query Match             48.6%;  Score 3048;  DB 14;  Length 1296;
  Best Local Similarity   49.0%;  Pred. No. 4.8e-242;
  Matches  610;  Conservative  192;  Mismatches  261;  Indels  182;  Gaps   17;

Qy        110 YTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIE 169
              :  |::|||  ::|| |:|| |||  || :|| ||:| | :| : | |  :|||||  : |
Db          2 FNPQLMIQTPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITE 61

Qy        170 NGMIEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF- 228
              | :: :|| |:||:|:|||||||||||||| |:||| |:| ::||| || : ||||
Db         62 TGYMDQIIEYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKIN 121

Qy        229 ASLEGFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSH 288
               :: : |:|:||:||  |: ||||:| |  || :||| :| :  ::|  |:|||||  |
Db        122 YQVDSWEEMLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSR 181

Qy        289 KFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQ 347
              |:|||||||::||  ::  |:|: | |||: | ||:|:|:||||:| :| :| | |:|::
Db        182 KYMHWQEELIVGGTVKNSTGKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDK 240

Qy        348 ASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLA 407
              |: :|:|||| :|::  ::: :|::|:: :|::|||||| :||:||  ||  |||||||
Db        241 AAAILEAWQRTYVEVVHQSVAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLA 300

Qy        408 YACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIG 467
              |||:||||||::|||:||||||||||:||:|||||:|:|:|||||||||||||||:|
Db        301 YACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVG 360

Qy        468 VDDVFLLAHAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALR 525
              ||||||||||:|       | ::| ||||:||| || ||||:|: || ||||:||||||
Db        361 VDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALR 420

Qy        526 AFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELG 585
              |||||||:||    |  |:|:||||||:|| ||  :|||: |||:||| ::|||: ||
Db        421 AFSLQAAVVVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYT 480

Qy        586 D-------GTVPVGIAH---------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP-- 627
              |       |  :|          : :|||  |  :  :    |  |:: :   |
Db        481 DTHDNTRYSPPPPYSSHSFAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVT 540

Qy        628 --SDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHA 685
                | |  :      ||||||  |  ::      |    || :| |: ||   :|| ||:  |
Db        541 VTQDTLSCQSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKA 598

Qy        686 KAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQG 745
              | :|: ||  |||:|||| | |:||| |||:||| |:|: |::|| :||| | : :|||
Db        599 KVVVIFLFLGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQK 658

Qy        746 GFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRI 805
              || : |  |:|||: ||::| |:      | |: ||||:|:||||:| ||| || :|:|
Db        659 A-DYPNIQHLLYDLHRSFSNVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKI 717

Qy        806 TRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVS 865
              ::|:|||:|| ||||||:|||   :|:| |||| ::||| :|:|  |  ||: || |||
Db        718 MPNNYKNGSDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVS 777

Qy        866 SDPLGLAASQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFV 924
              :||:  |||||  |  |||:||| |   |  |||| |:|:|:||||| | ||: |:|||
Db        778 NDPVAYAASQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFV 837

Qy        925 EAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLL 984
              ||||  |  |:      |: :||:| |||||||:|||   || : ::| |||||||: ||
Db        838 EAIEKVRTICSNYTSLGLSSYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLL 897

Qy        985 NPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQ 1044
              ||||||:||:|||:|||||||:|| :||||||:|||||:|||||||||||||||| |||
Db        898 NPWTAGIIVMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAI 957

Qy       1045 GSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGL 1104
                :| ||  |||| |||| |||:|||||:|||||| |||||||||| | :||:||:|:||
Db        958 SDKNRRAVLALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGL 1017

Qy       1105 VLLPVLLSILGPPPEV---------------------------------------------- 1120
              ||||||||  || |||
Db       1018 VLLPVLLSFFGPYPEVSPANGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQ 1077

Qy       1121 ---------IQMY-----------------------------------------KESPEI 1130
                      :: |                                          |: | :
Db       1078 TTVSGLSEELRHYEAQQGAGGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPKQQPHL 1137

Qy       1131 LS---PPAPQG---------GGL--------------------------RWG--------- 1144
                |   ||  ||           ||                        |||
Db       1138 DSGSLPPGRQGQQPRRDPPRKGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHN 1197

Qy       1145 --------ASSSLPQSFARVTT-----SMTVAIHPPPLPGAYIHP 1176
                       ||:|     :||     |:|||:||||:||   :|
Db       1198 PRNPTSTAMGSSVPGYCQPITTVTASASVTVAVHPPPVPGPGRNP 1242


RESULT 12
US-08-954-701A-4
; Sequence 4, Application US/08954701A
; Publication No. US20030032085A1
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,701A
;      FILING DATE:  20-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36709
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1311 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-954-701A-4

  Query Match             35.6%;  Score 2235;  DB 8;  Length 1311;
  Best Local Similarity   39.9%;  Pred. No. 7.5e-175;
  Matches  470;  Conservative  213;  Mismatches  402;  Indels   94;  Gaps   19;

Qy         18 ARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGALALGLR 74
                |  |  ::  |::   :  ||:||: |  || ||| :|   |||||: :|      :||:
Db         41 AALALSELEKGNIEGGRTSLWIRAWLQEQLFILGCFLQGDAGKVLFVAILVLSTFCVGLK 100
```





RESULT 13
US-09-754-032-4
; Sequence 4, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-754-032-4

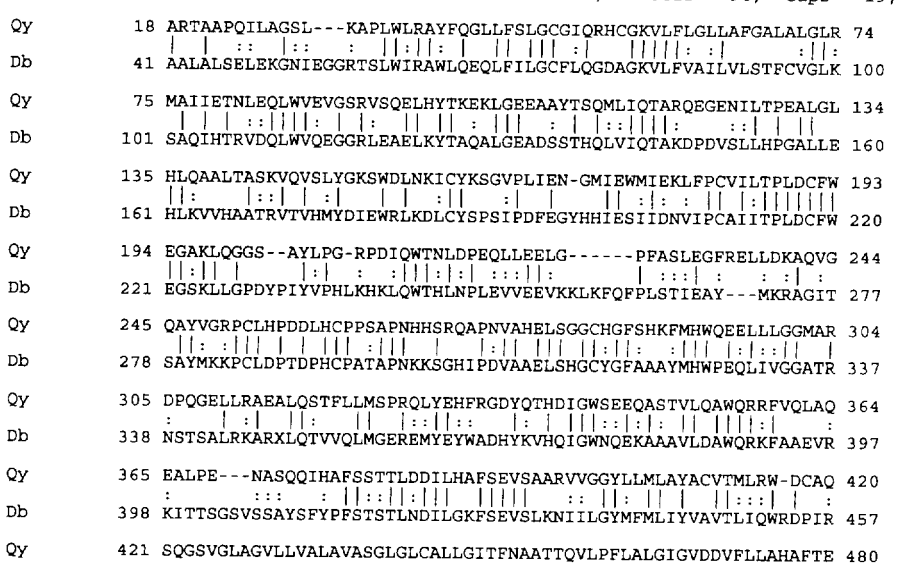
Query Match 35.6%; Score 2235; DB 10; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;



RESULT 14
US-10-421-446-4
; Sequence 4, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-421-446-4

Query Match 35.6%; Score 2235; DB 14; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;



```
Db        458 SQAGVGIAGVLLLSITVAAGLGFCALLGIPFNASSTQIVPFLALGLGVQDMFLLTHTYVE 517

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        518 QAGDVPREERTGLVLKKSGLSVLLASLCNVMAFLAAALLPIPAFRVFCLQAAILLLFNLG 577

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCF--SSPCSAQVIQILPQELGDGTVPVGIAHLTA 598

Db        578 SILLVFPAMISLDLRRRSAARADLLCCLMPESP--------LPKK----KIP-------- 617

Qy        599 TVQAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAAC 658

Db        618 ------------ERAKTRKNDKTHRIDTTRQPLDPDV--------------SENVTKTCC 651

Qy        659 KSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVP 718

Db        652 LSVSLTKW-----AKNQYAPFIMRPAVKVTSMLALIAVILTLSVWGATKVKDGLDLTDIVP 706

Qy        719 RGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAP 778

Db        707 ENTDEHEFLSRQEKYFGFYNMYAVTQGNFEYPTNQKLLYEYHDQFVRIPNIIKNDNGGLT 766

Qy        779 RTWLHYYRNWLQGIQAAFDQDWASGRITRHSY-RNGSEDGALAYKLLIQTGDAQEPLDFS 837

Db        767 KFWLSLFRDWLLDLQVAFDKEVASGCITQEYWCKNASDEGILAYKLMVQTGHVDNPIDKS 826

Qy        838 QLTT-RKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGEN 896

Db        827 LITAGHRLVDKDGIINPKAFYNYLSAWATNDALAYGASQGNLKPQPQRWIHSPEDV---H 883

Qy        897 LRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQ 956

Db        884 LEIKKSSPLIYTQLPFYLSGLSDTXSIKTLIRSVRDLCLKYEAKGLPNFPSGIPFLFWEQ 943

Qy        957 YLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSA 1016

Db        944 YLYLRTSLLLALACALAAVFIAVMVLLLNAWAAVLVTLALATLVLQLLGVMALLGVKLSA 1003

Qy       1017 IPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLML 1076

Db       1004 MPAVLLVLAIGRGVHFTVHLCLGFVTSIGCKRRRASLALESVLAPVVHGALAAALAASML 1063

Qy       1077 AGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAP 1136

Db       1064 AASECGFVARLFLRLLLDIVFLGLIDGLLFFPIVLSILGPAAEVRPI--EHPERLSTPSP 1121

Qy       1137 Q--------------GGGLRWGASSSLPQSFARVTTSMT 1161

Db       1122 KCSPIHPRKSSSSSGGGDKSSRTSKSAPRPCAPSLTTIT 1160
```

RESULT 15
US-09-898-533-3
; Sequence 3, Application US/09898533
; Patent No. US20020106656A1
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
; TITLE OF INVENTION: PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/898,533
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: US/09/268,140
; PRIOR FILING DATE: 2000-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-898-533-3

Query Match 31.8%; Score 1992; DB 9; Length 1286;
Best Local Similarity 37.4%; Pred. No. 8.8e-155;
Matches 429; Conservative 226; Mismatches 411; Indels 80; Gaps 19;

```
Qy         18 ARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGALALGLR 74

Db         34 AQVALDQIDKGKARGSRTAIYLRSVFQSHLETLGSSVQKHAGKVLFVAILVLSTFCVGLK 93

Qy         75 MAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILTPEALGL 134

Db         94 SAQIHSKVHQLWIQEGGRLEAELAYTQKTIGEDESATHQLLIQTTHDPNASVLHPQALLA 153

Qy        135 HLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIEN-GMIEWMIEKLFPCVILTPLDCFW 193

Db        154 HLEVLVKATAVKVHLYDTEWGLRDMCNMPSTPSFEGIYYIEQILRHLIPCSIITPLDCFW 213

Qy        194 EGAKLQG--GSAYLPG-RPDIQWTNLDP--------EQLLEELGPFASLEGFRELLDKAQ 242

Db        214 EGSQLLGPESAVVIPGLNQRLLWTTLNPASVMQYMKQKMSEEKISF-DFETVEQYMKRAA 272

Qy        243 VGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGM 302

Db        273 IGSGYMEKPCLNPLNPNCPDTAPNKNSTQPPDVGAILSGGCYGYAAKHMHWPEELIVGGR 332

Qy        303 ARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQL 362

Db        333 KRNRSGHLRKAQALQSVVQLMTEKEMYDQWQDNYKVHHLGWTQEKAAEVLNAWQRNFSRE 392

Qy        363 AQEALPENA----SQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRW-D 417

Db        393 VEQLLRKQSRIATNYDIYVFSSAALDDILAKFSHPSALSIVIGVAVTVLYAFCTLLRWRD 452

Qy        418 CAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHA 477

Db        453 PVRGQSSVGVAGVLLMCFSTAAGLGLSALLGIVFNAASTQVVPFLALGLGVDHIFMLTAA 512

Qy        478 FTEALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGC 537

Db        513 YAE----SNRREQTKLILKKVGPSILFSACSTAGSFFAAAFIPVPALKVFCLQAAIVMCS 568

Qy        538 TFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQ---VIQILPQELGDGTVPVGIA 594

Db        569 NLAAAALLVFPAMISLDLRRRTAGRADIFCCCFPVWKEQPKVAPPVLPLNNNNG------- 621

Qy        595 HLTATVQAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQ 654

Db        622 ------RGARHPKSCNNNRVPL---------PAQNPLLEQRADIPGSSHSL--------- 657

Qy        655 KAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALT 714

Db        658 ---------ASFSLATFAFQHYTPFLMRSWVKFLTVMGFLAALISSLYASTRLQDGLDII 708

Qy        715 DVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPA 774

Db        709 DLVPKDSNEHKFLDAQTRLFGFYSMYAVTQGNFEYPTQQQLLRDYHDSFVRVPHVIKNDN 768

Qy        775 TQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHS-YRNGSEDGALAYKLLIQTGDAQEP 833

Db        769 GGLPDFWLLLFSEWLGNLQKIFDEEYRDGRLTKECWFPNASSDAILAYKLIVQTGHVDNP 828

Qy        834 LDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLH--DKYD 891

Db        829 VDKELVLTNRLVNSDGIINQRAFYNYLSAWATNDVFAYGASQGKLYPEPRQYFHQPNEYD 888

Qy        892 TTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPF 951

Db        889 -----LKIPKSLPLVYAQMPFYLHGLTDTSQIKTLIGHIRDLSVKYEGFGLPNYPSGIPF 943

Qy        952 LFWEQYLGLRRCF-LLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFL 1010

Db        944 IFWEQYMTLRSSLAMILACVLLAALVLV-SLLLLSVWAAVLVILSVLASLAQIFGAMTLL 1002
```

```
Qy       1011 GIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTL 1070
Db       1003 GIKLSAIPAVILILSVGMMLCFNVLISLGFMTSVGNRQRRVQLSMQMSLGPLVHGMLTSG 1062

Qy       1071 LGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEI 1130
Db       1063 VAVFMLSTSPFEFVIRHFCWLLLVVLCVGACNSLLVFPILLSMVGPEAELVPL--EHPDR 1120

Qy       1131 LSPPAP 1136
Db       1121 ISTPSP 1126
```

Search completed: November 22, 2004, 08:08:02
Job time : 335 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 22, 2004, 07:45:05 ; Search time 24 Seconds
(without alignments)
3324.190 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	1203	3	US-09-293-505-2	Sequence 2, Appli
2	6272	100.0	1203	4	US-09-060-939A-2	Sequence 2, Appli
3	6248	99.6	1203	3	US-09-207-857-2	Sequence 2, Appli
4	6248	99.6	1203	4	US-09-909-280A-2	Sequence 2, Appli
5	5599	89.3	1182	3	US-09-293-505-7	Sequence 7, Appli
6	5599	89.3	1182	4	US-09-060-939A-7	Sequence 7, Appli
7	3348	53.4	1447	2	US-08-540-406-19	Sequence 19, Appl
8	3348	53.4	1447	3	US-08-656-055-19	Sequence 19, Appl
9	3348	53.4	1447	3	US-08-954-668-19	Sequence 19, Appl
10	3348	53.4	1447	3	US-09-268-140-5	Sequence 5, Appli
11	3348	53.4	1447	4	US-08-918-658-19	Sequence 19, Appl
12	3348	53.4	1447	4	US-09-724-631-19	Sequence 19, Appl
13	3348	53.4	1447	4	US-08-954-701A-19	Sequence 19, Appl
14	3348	53.4	1447	5	PCT-US95-13233-19	Sequence 19, Appl
15	3337	53.2	1434	2	US-08-540-406-10	Sequence 10, Appl
16	3337	53.2	1434	3	US-08-656-055-10	Sequence 10, Appl
17	3337	53.2	1434	3	US-08-954-668-10	Sequence 10, Appl
18	3337	53.2	1434	4	US-08-918-658-10	Sequence 10, Appl
19	3337	53.2	1434	4	US-09-724-631-10	Sequence 10, Appl
20	3337	53.2	1434	4	US-08-954-701A-10	Sequence 10, Appl
21	3337	53.2	1434	5	PCT-US95-13233-10	Sequence 10, Appl
22	3048	48.6	1296	4	US-08-857-636-60	Sequence 60, Appl
23	2627	41.9	529	3	US-09-500-063-2	Sequence 2, Appli
24	2235	35.6	1311	2	US-08-540-406-4	Sequence 4, Appli
25	2235	35.6	1311	3	US-08-656-055-4	Sequence 4, Appli
26	2235	35.6	1311	3	US-08-954-668-4	Sequence 4, Appli
27	2235	35.6	1311	4	US-08-918-658-4	Sequence 4, Appli
28	2235	35.6	1311	4	US-09-724-631-4	Sequence 4, Appli
29	2235	35.6	1311	4	US-08-954-701A-4	Sequence 4, Appli
30	2235	35.6	1311	5	PCT-US95-13233-4	Sequence 4, Appli
31	1992	31.8	1286	3	US-09-268-140-3	Sequence 3, Appli
32	1961.5	31.3	1299	3	US-08-460-900C-62	Sequence 62, Appl
33	1961.5	31.3	1299	3	US-08-674-509B-48	Sequence 48, Appl
34	1961.5	31.3	1299	3	US-08-954-698-48	Sequence 48, Appl
35	1961.5	31.3	1299	4	US-09-639-695-62	Sequence 62, Appl
36	1961.5	31.3	1299	4	US-09-448-188-48	Sequence 48, Appl
37	1961.5	31.3	1299	4	US-08-954-128-48	Sequence 48, Appl
38	1961.5	31.3	1299	4	US-08-954-740-48	Sequence 48, Appl
39	1936.5	30.9	1285	2	US-08-540-406-6	Sequence 6, Appli
40	1936.5	30.9	1285	3	US-08-656-055-6	Sequence 6, Appli
41	1936.5	30.9	1285	3	US-08-954-668-6	Sequence 6, Appli
42	1936.5	30.9	1285	4	US-08-918-658-6	Sequence 6, Appli
43	1936.5	30.9	1285	4	US-09-724-631-6	Sequence 6, Appli
44	1936.5	30.9	1285	4	US-08-954-701A-6	Sequence 6, Appli
45	1936.5	30.9	1285	5	PCT-US95-13233-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-293-505-2
; Sequence 2, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-505-2

Query Match 100.0%; Score 6272; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

```
RESULT 2
US-09-060-939A-2
; Sequence 2, Application US/09060939A
; Patent No. 6709838
;  GENERAL INFORMATION:
;    APPLICANT:  Frederic de Sauvage, David A. Carpenter
;    TITLE OF INVENTION:  Patched-2
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,939A
;      FILING DATE:  15-Apr-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1405
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1203 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-060-939A-2

  Query Match           100.0%;  Score 6272;  DB 4;  Length 1203;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
```

```
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203

Db       1201 ATG 1203
```

RESULT 3
US-09-207-857-2
; Sequence 2, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: human
US-09-207-857-2

Query Match 99.6%; Score 6248; DB 3; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Db        541 AVMLVFPAIFSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWMAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203

Db       1201 ATG 1203
```

```
RESULT 4
US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
;  APPLICANT: Bumcroft, David A.
;  TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
;  TITLE OF INVENTION:  THERETO
;  FILE REFERENCE: CIBT-P02-050
;  CURRENT APPLICATION NUMBER: US/09/909,280A
;  CURRENT FILING DATE:  2001-07-19
;  PRIOR APPLICATION NUMBER: US 09/207,857
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: US 60/067,940
;  PRIOR FILING DATE: 1997-12-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1203
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-909-280A-2

  Query Match             99.6%;  Score 6248;  DB 4;  Length 1203;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAIFSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWMAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203


RESULT 5
US-09-293-505-7
; Sequence 7, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
;  APPLICANT: de Sauvage, Frederic
;  APPLICANT: Carpenter, David A.
;  TITLE OF INVENTION: Patched-2
;  FILE REFERENCE: P1405R1
;  CURRENT APPLICATION NUMBER: US/09/293,505
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: US 60/081,884
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
;   LENGTH: 1182
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-293-505-7

  Query Match             89.3%;  Score 5599;  DB 3;  Length 1182;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 1074;  Conservative   43;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              | |   | ||||||||||||:|| |||||:||||||||||||||||| ||:|||||||
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              |||:|||||||||:|:|||:|||||||||||||||||||||||||||||||||||||||||
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120
```

```
Qy      121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
Db      121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy      181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db      181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy      241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db      241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy      301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db      301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy      361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db      361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420

Qy      421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db      421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480

Qy      481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db      481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540

Qy      541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db      541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600

Qy      601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db      601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660

Qy      661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db      661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy      721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db      721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy      781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db      781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840

Qy      841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db      841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy      901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db      901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy      961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db      961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy     1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db     1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080

Qy     1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db     1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140

Qy     1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
Db     1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181
```

```
RESULT 6
US-09-060-939A-7
; Sequence 7, Application US/09060939A
; Patent No. 6709838
;  GENERAL INFORMATION:
;    APPLICANT:  Frederic de Sauvage, David A. Carpenter
;    TITLE OF INVENTION:  Patched-2
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,939A
;      FILING DATE:  15-Apr-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1405
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-060-939A-7

  Query Match             89.3%;  Score 5599;  DB 4;  Length 1182;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 1074;  Conservative   43;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db        421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480
```

```
Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db        481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db        541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db        601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db        661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db        781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db        841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db        901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db        961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db       1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db       1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
Db       1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181
```

```
RESULT 7
US-08-540-406-19
; Sequence 19, Application US/08540406
; Patent No. 5837538
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/540,406
;      FILING DATE:  06-OCT-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1447 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-540-406-19

  Query Match             53.4%;  Score 3348;  DB 2;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;
```

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
```

```
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824

Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884

Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943

Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003

Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063

Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121

Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139

Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140

Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 -----------------------------LRWG----------------ASSSLPQSFAR 1155

Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 8
US-08-656-055-19
; Sequence 19, Application US/08656055
; Patent No. 6027882
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,055
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/540,406
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1447 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-656-055-19

  Query Match             53.4%;  Score 3348;  DB 3;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68

Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128

Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188

Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247

Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307

Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366

Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426

Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484

Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544

Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595

Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644

Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704

Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764

Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
```

```
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884

Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943

Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003

Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063

Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121

Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139

Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140

Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 -----------------------------LRWG----------------ASSSLPQSFAR 1155

Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 9
US-08-954-668-19
; Sequence 19, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-954-668-19

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68

Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIPGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128

Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188

Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247

Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307

Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366

Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426

Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484

Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544

Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595

Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644

Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704

Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764

Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824

Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884

Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
```

```
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003

Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063

Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121

Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139

Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140

Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 -----------------------------LRWG----------------ASSSLPQSFAR 1155

Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 10
US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
;  APPLICANT:  Gemmill, Robert M.
;  APPLICANT:  Drabkin, Harry A.
;  TITLE OF INVENTION:  TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
;  FILE REFERENCE:  93445-00004
;  CURRENT APPLICATION NUMBER: US/09/268,140
;  CURRENT FILING DATE:  2000-03-12
;  PRIOR APPLICATION NUMBER:  US 60/077,723
;  PRIOR FILING DATE:  1998-03-12
;  NUMBER OF SEQ ID NOS:  46
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-268-140-5

  Query Match           53.4%;  Score 3348;  DB 3;  Length 1447;
  Best Local Similarity  49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68

Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128

Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188

Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247

Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307

Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366

Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426

Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484

Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544

Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595

Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644

Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704

Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764

Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824

Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884

Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943

Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003

Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063

Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121

Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139

Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140

Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 -----------------------------LRWG----------------ASSSLPQSFAR 1155

Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
```

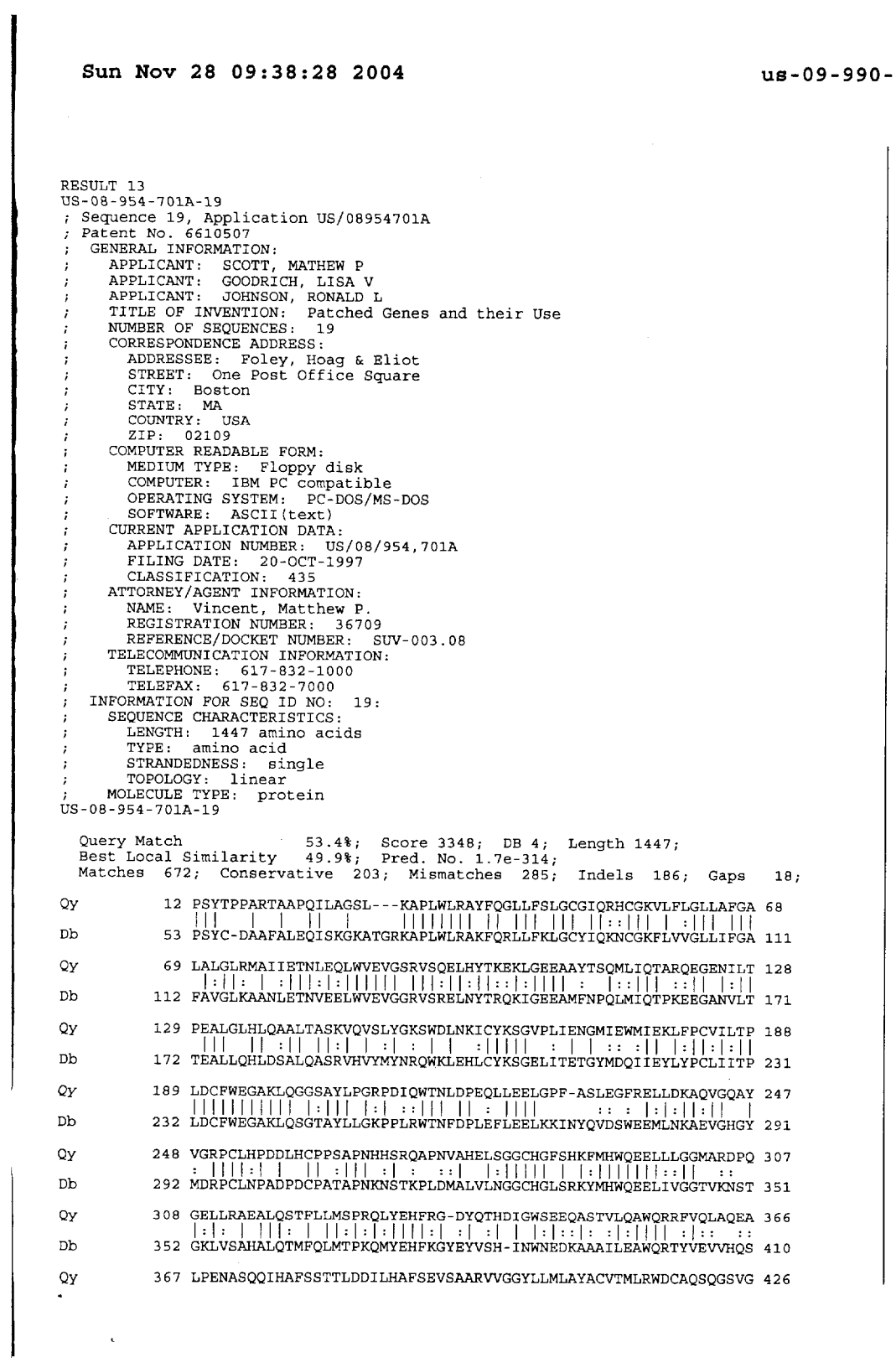
```
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 11
US-08-918-658-19
; Sequence 19, Application US/08918658
; Patent No. 6429354
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/918,658
;             FILING DATE: 22-Aug-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/656,055
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/540,406
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1447 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-918-658-19

  Query Match             53.4%;  Score 3348;  DB 4;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:|  | :|  : | |  :|||||  : | | :: :|| |:||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||| |:||| |:| ::||| || : ||||      :: : |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
```

```
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||||| :||:||  ||  |||||||||||:|||||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
               |||||||||:||:|||||:|:||:||||||||||||||:|||||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:||||||||||||:||    |  |:|
Db         531 IPPEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |   :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :     |   |:: :   |      | |  :       ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::     |    || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |  |:     |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| |||||||:|||   || : ::| |||||||: |||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :||||||:|||||:|||||||||||||||| |||  | :|  ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                   ::   |||          ||                             | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140
               |
Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                 ||:|
Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
               :||     |:|||:|||||:||   :|
```

```
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 12
US-09-724-631-19
; Sequence 19, Application US/09724631
; Patent No. 6551782
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/724,631
;             FILING DATE: 28-No. 6551782-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/656,055
;             FILING DATE: 1996-05-31
;             APPLICATION NUMBER: 08/540,406
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1447 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-724-631-19

  Query Match             53.4%;  Score 3348;  DB 4;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
              |||||||||| |:||| |:| ::||| || : ||||      :: : |:|:||:||  |
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
              : ||||:| |  || :||| :| :  ::|  |:|||| | |:||||||::||  ::

Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
              |:|: | |||: | ||:|:|:|:|||:| :| :| | |:|::|: :|:|||| :|::  ::
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
              : :|::|:: :|::|||||||| :||:|| || ||||||||||:|||||||::|||:||
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLLAHAFTEALPG-- 484
              |||||||||:||:|||||:|:||:|||||||||||||||:|||||||||||:|
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   |  |:|
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
              :|||||:|| ||  :|||: |||:||| ::|||: ||   |          |   :|
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   ||:: :   |   | | :      ||||
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
              || |  ::     |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
              | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
              ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
              :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
              |:||| |   |  |||| |:|:|:||||| | ||: |:|||||| |  |:     |:
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
              :||:| ||||||||:|||   || : ::| |||||||: |||||||:|:|:|||:|||||
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
              ||:|| :||||||:|||||:|||||||||||||| |||  | :| ||  |||| ||||
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
              |||:|||||:|||||| |||||||||| | :||:||:|:||||||||  || |||
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                  ::   |||          ||                             | ||
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
              |
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                          |||                ||:|
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
              :||     |:|||:||||:||   :|
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 13
US-08-954-701A-19
; Sequence 19, Application US/08954701A
; Patent No. 6610507
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;



RESULT 14
PCT-US95-13233-19
; Sequence 19, Application PC/TUS9513233
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY

```
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13233
;      FILING DATE:  06-OCT-1990
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1447 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-13233-19

  Query Match             53.4%;  Score 3348;  DB 5;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.7e-314;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-------------------------------APQGG 1139
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G---------------------------------------------------------- 1140
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG---------------ASSSLPQSFAR 1155
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393


RESULT 15
US-08-540-406-10
; Sequence 10, Application US/08540406
; Patent No. 5837538
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
```

```
;       COUNTRY:  US
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/540,406
;       FILING DATE:  06-OCT-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Rowland, Bertram I
;       REGISTRATION NUMBER:  20015
;       REFERENCE/DOCKET NUMBER:  a60190-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-781-1989
;       TELEFAX:  415-398-3249
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1434 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-540-406-10

  Query Match             53.2%;  Score 3337;  DB 2;  Length 1434;
  Best Local Similarity   53.1%;  Pred. No. 1.9e-313;
  Matches  672;  Conservative  206;  Mismatches  309;  Indels   78;  Gaps   20;

Qy          3 RSPPLREL--PPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGK 57
              |: | |:    |||   | | ||  |     |||||||| || ||| ||| ||::|||
Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86

Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
               | :||| ||| |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||
Db         87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy        118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177
               | ::|| |:|| |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|
Db        147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy        178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236
               | |:||:|:|||||||||||||| |:||| |:| ::||| || : ||||      :: : |
Db        207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy        237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296
               :|:||:||  |: ||||:| |  || :||| :| :  :||  |:||| | | |:||||||
Db        267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy        297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355
               |::||  ::  |:|: | |||: | ||:|:|:|||||| || :| | |:|::|: :|:||
Db        327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy        356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415
               || :|::  :::  |::|::  |::|||||| :||:||  ||  ||||||||||:||||
Db        386 QRTYVEVVHQSVAPNSTQKVLPFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445

Qy        416 WDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLA 475
               |||::|||:|||||||||||:||:|||||:|:||:|||||||||||||||:|||||||||
Db        446 WDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLA 505

Qy        476 HAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533
               |||:|       | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:
Db        506 HAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAV 565

Qy        534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------- 586
               ||   |  |:|:||||||:|| ||  :|||: |||:||| ::|||: ||   :
Db        566 VVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTEPHSNTRY 625

Qy        587 GTVPVGIAH---------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS 633
                  |   :|         : :|||  |  :  :    |   |:: :   |     | |

Db        626 SPPPPYTSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDNLSC 685

Qy        634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLF 693
               :      ||||||  |  ::      |   || :| |: ||   :|| ||:  || :|::||
Db        686 QSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVILLF 743

Qy        694 GALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQ 753
               |||:|||| | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |
Db        744 LGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQ 802

Qy        754 RALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNG 813
               |:|||: ||::| |:      | |: ||||:|:||||:| ||| || :|||  ::|:||
Db        803 HLLYDLHKSFSNVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNNYKNG 862

Qy        814 SEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAA 873
               |:|| ||||||:|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||
Db        863 SDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAA 922

Qy        874 SQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA 932
               |||| | |||:||| |  | |||| |:|:|:||||| | ||: |:|||||  |
Db        923 SQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRV 982

Qy        933 ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLI 992
               |      |: :||:| ||||||||: ||   ||:: ::| |||||||: |||||||:|
Db        983 ICNNYTSLGLSSYPNGYPFLFWEQYISLRHWLLLSISVVLACTFLVCAVFLLNPWTAGII 1042

Qy        993 VLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAA 1052
               |:|||:|||||||:|| :||||||:|||||:|||||||||||||| ||| | :| ||
Db       1043 VMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNHRAM 1102

Qy       1053 HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLS 1112
               |||| |||| |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||
Db       1103 LALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPVLLS 1162

Qy       1113 ILGPPPEVI------QMYKESPEILSPP-----APQGGGLRWGASSSLPQSFARVTTS-- 1159
                || |||      ::   |||   ||      |    |    |: ||  :  :: | |
Db       1163 FFGPCPEVSPANGLNRLPTPSPE--PPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220

Qy       1160 --------------------MTVAIHPPPLPGAYIHP-APDEPPWSPAA---TSSGNLS 1194
                                   :    :|       :|| :  :|| :|       ||:||
Db       1221 SEELRQYEAQQGAGGPAHQVIVEATENPVFARSTVVHPDSRHQPPLTPRQQPHLDSGSLS 1280

Qy       1195 SRGPG 1199
                ||
Db       1281 ---PG 1282


Search completed: November 22, 2004, 07:58:45
Job time : 34 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:26 ; Search time 155 Seconds
(without alignments)
5516.639 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09990046/runat_21112004_130920_18563/app_query.fasta_1.1351
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990046_@CGN_1_1_62_@runat_21112004_130920_18563 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	4030	3	US-09-293-505-1	Sequence 1, Appli
2	6272	100.0	4030	4	US-09-060-939A-1	Sequence 1, Appli
3	6248	99.6	4391	3	US-09-207-857-1	Sequence 1, Appli
4	6248	99.6	4391	4	US-09-909-280A-1	Sequence 1, Appli
5	3955	63.1	4004	3	US-09-293-505-8	Sequence 8, Appli
6	3955	63.1	4004	4	US-09-060-939A-8	Sequence 8, Appli
7	3387	54.0	2082	3	US-09-293-505-9	Sequence 9, Appli
8	3387	54.0	2082	4	US-09-060-939A-9	Sequence 9, Appli
9	3349	53.4	5288	2	US-08-540-406-18	Sequence 18, Appl
10	3349	53.4	5288	3	US-08-656-055-18	Sequence 18, Appl
11	3349	53.4	5288	3	US-08-954-668-18	Sequence 18, Appl
12	3349	53.4	5288	4	US-08-918-658-18	Sequence 18, Appl
13	3349	53.4	5288	4	US-09-724-631-18	Sequence 18, Appl
14	3349	53.4	5288	4	US-08-954-701A-18	Sequence 18, Appl
15	3349	53.4	5288	5	PCT-US95-13233-18	Sequence 18, Appl
16	3337	53.2	5187	2	US-08-540-406-3	Sequence 3, Appli
17	3337	53.2	5187	2	US-08-540-406-9	Sequence 9, Appli
18	3337	53.2	5187	3	US-08-656-055-3	Sequence 3, Appli
19	3337	53.2	5187	3	US-08-656-055-9	Sequence 9, Appli
20	3337	53.2	5187	3	US-08-954-668-3	Sequence 3, Appli
21	3337	53.2	5187	3	US-08-954-668-9	Sequence 9, Appli
22	3337	53.2	5187	4	US-08-918-658-3	Sequence 3, Appli
23	3337	53.2	5187	4	US-08-918-658-9	Sequence 9, Appli
24	3337	53.2	5187	4	US-09-724-631-3	Sequence 3, Appli
25	3337	53.2	5187	4	US-09-724-631-9	Sequence 9, Appli
26	3337	53.2	5187	4	US-08-954-701A-3	Sequence 3, Appli
27	3337	53.2	5187	4	US-08-954-701A-9	Sequence 9, Appli
28	3337	53.2	5187	5	PCT-US95-13233-3	Sequence 3, Appli
29	3337	53.2	5187	5	PCT-US95-13233-9	Sequence 9, Appli
30	3336	53.2	6568	4	US-08-857-636-1	Sequence 1, Appli
31	2797.5	44.6	2032	3	US-09-500-063-1	Sequence 1, Appli
32	1972.5	31.4	3900	2	US-08-356-060A-42	Sequence 42, Appl
33	1972.5	31.4	3900	3	US-08-460-900C-42	Sequence 42, Appl
34	1972.5	31.4	3900	3	US-08-674-509B-42	Sequence 42, Appl
35	1972.5	31.4	3900	3	US-08-954-698-42	Sequence 42, Appl
36	1972.5	31.4	3900	3	US-08-957-874-42	Sequence 42, Appl
37	1972.5	31.4	3900	4	US-09-639-695-42	Sequence 42, Appl
38	1972.5	31.4	3900	4	US-09-448-188-42	Sequence 42, Appl
39	1972.5	31.4	3900	4	US-08-954-128-42	Sequence 42, Appl
40	1972.5	31.4	3900	4	US-08-954-740-42	Sequence 42, Appl
41	1972.5	31.4	3900	4	US-09-736-476-42	Sequence 42, Appl
42	1956	31.2	4434	2	US-08-540-406-5	Sequence 5, Appli
43	1956	31.2	4434	3	US-08-656-055-5	Sequence 5, Appli
44	1956	31.2	4434	3	US-08-954-668-5	Sequence 5, Appli
45	1956	31.2	4434	4	US-08-918-658-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-293-505-1
; Sequence 1, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-293-505-1

Alignment Scores:

Pred. No.:	0	Length:	4030
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-293-505-1 (1-4030)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352
Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe  60
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412
Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr  80
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472
Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532
Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592
Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652
Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712
Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772
Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db        773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832
Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db        833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db        893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db        953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012
Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072
Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132
Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312
Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372
Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492
Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552
Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db       1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db       1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672
Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db       1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db       1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792
Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db       1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972
Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512
```

```
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932

Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3833 GCCACTGGG 3841
```

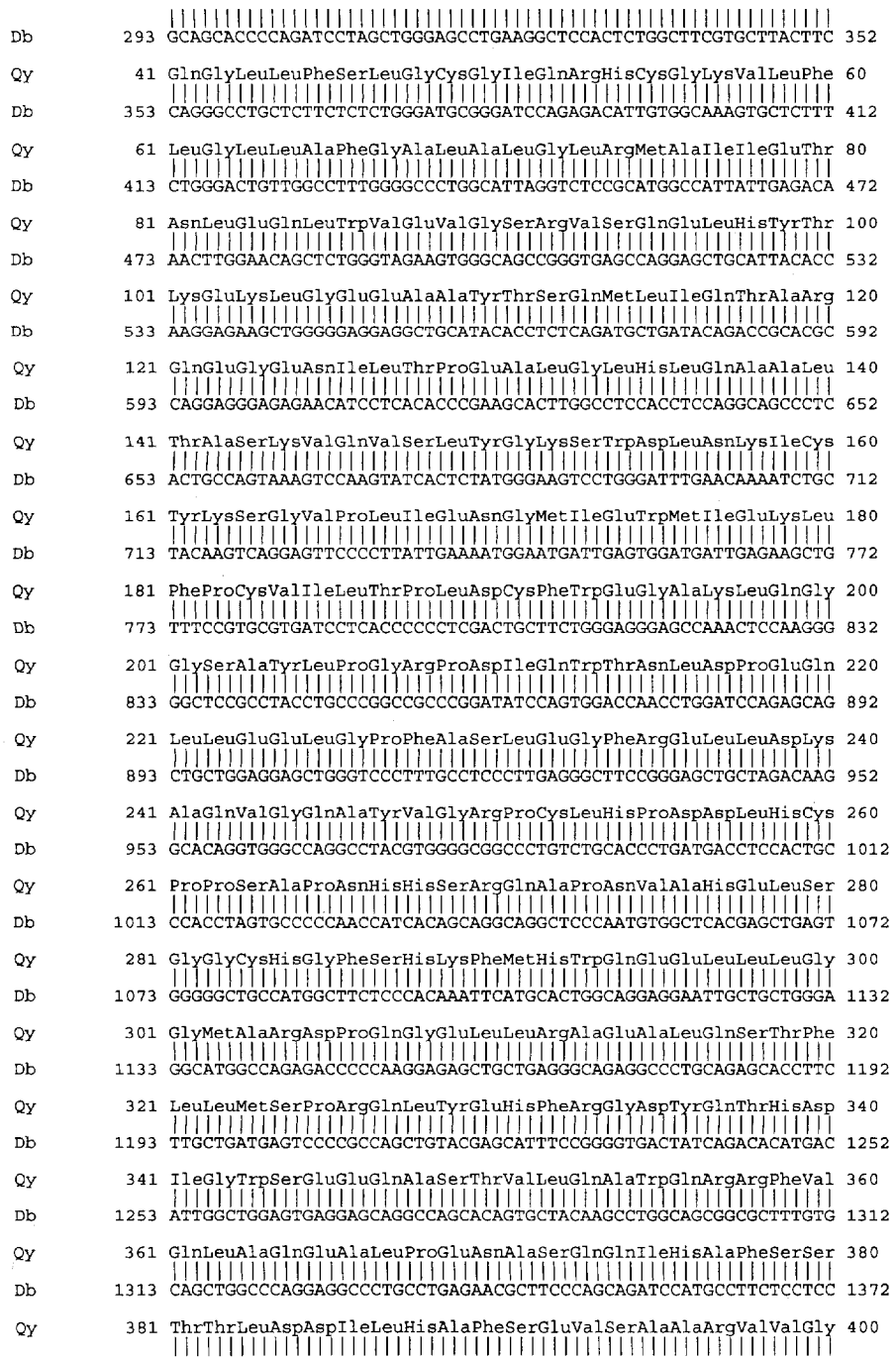
RESULT 2
US-09-060-939A-1
; Sequence 1, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4030 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-060-939A-1

Alignment Scores:

Pred. No.:	0	Length:	4030
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-060-939A-1 (1-4030)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
```


Db 293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352
Qy 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412
Qy 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db 413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472
Qy 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532
Qy 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592
Qy 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db 593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652
Qy 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712
Qy 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772
Qy 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832
Qy 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
Qy 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372
Qy 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432
Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512

```
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932

Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3833 GCCACTGGG 3841
```

RESULT 3
US-09-207-857-1
; Sequence 1, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-207-857-1

Alignment Scores:

Pred. No.:	0	Length:	4391
Score:	6248.00	Matches:	1200
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	3	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-207-857-1 (1-4391)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
```

```
Db        597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656
Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db        657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716
Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db        717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776
Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db        777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836
Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db        837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896
Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db        897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956
Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db        957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016
Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db       1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076
Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136
Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196
Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256
Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316
Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db       1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376
Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db       1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436
Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db       1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496
Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db       1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556
Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db       1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616
Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db       1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676
Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db       1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736
Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db       1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796
Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db       1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856
Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db       1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916
Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976
Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036
Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636
Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696
Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756
Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816
```

```
Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876

Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936

Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db      2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996

Qy       901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056

Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776

Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836

Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy      1201 AlaThrGly 1203
Db      3897 GCCACTGGG 3905
```

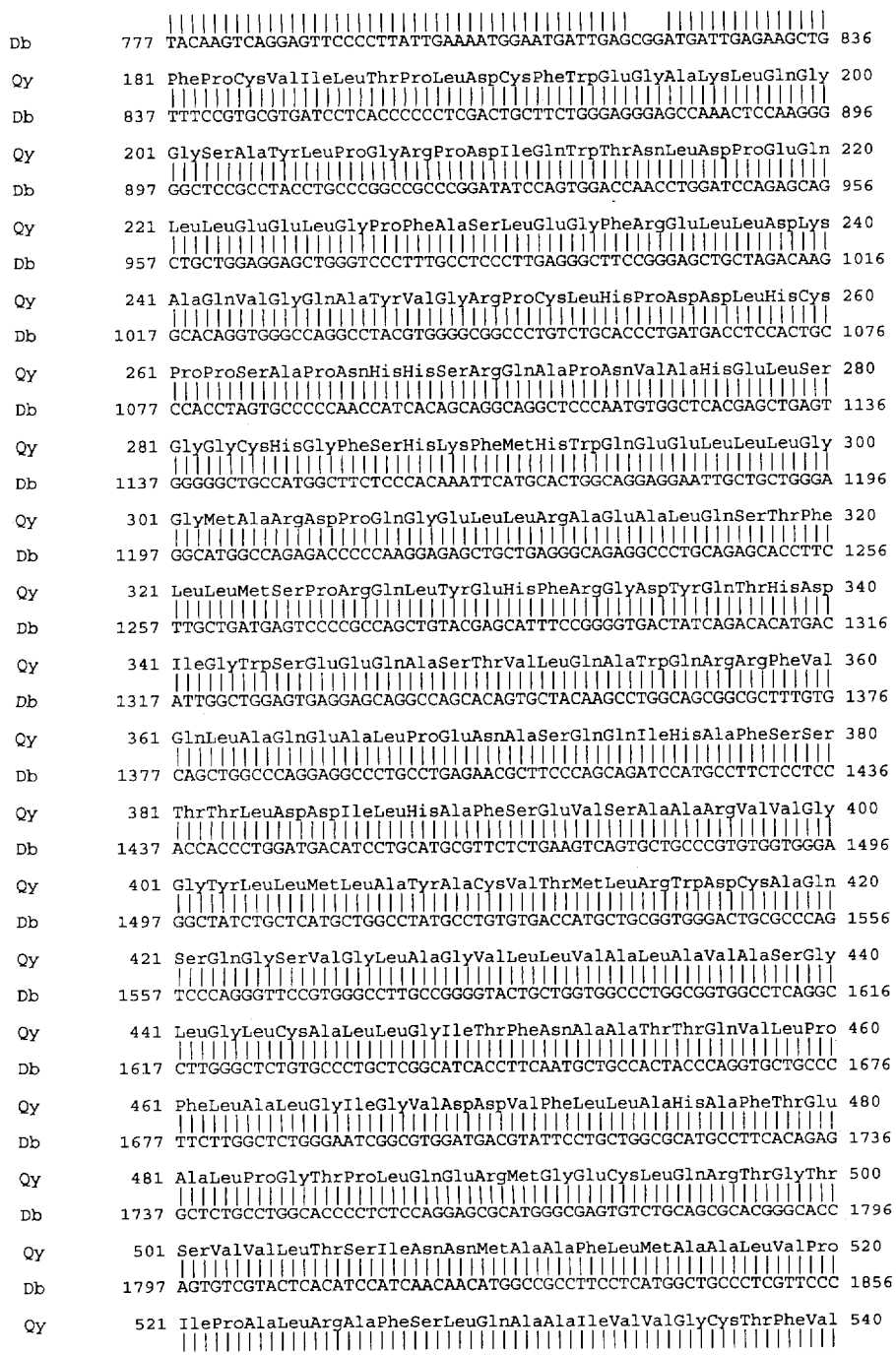
RESULT 4
US-09-909-280A-1
; Sequence 1, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-909-280A-1

Alignment Scores:

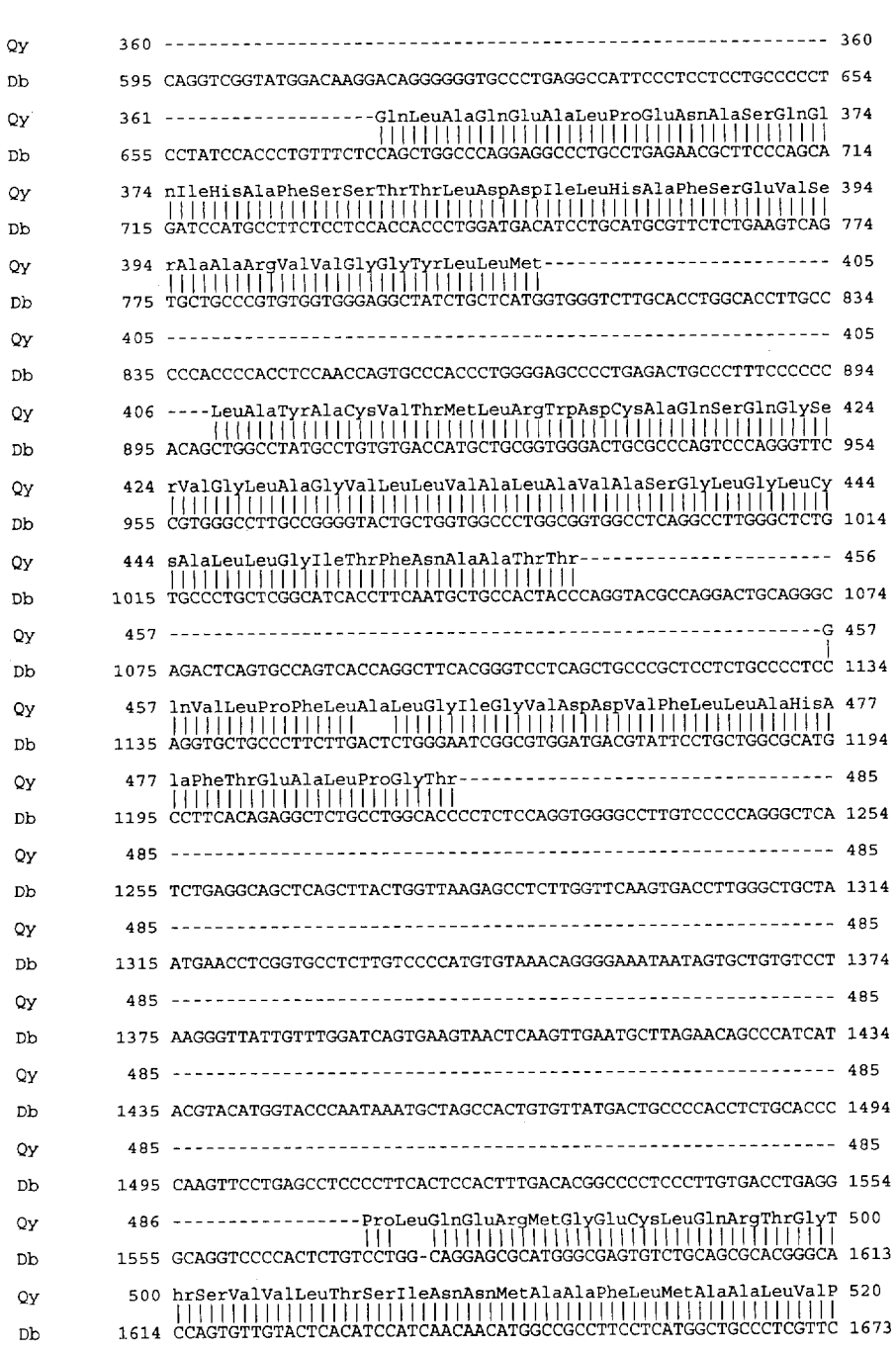
Pred. No.:	0	Length:	4391
Score:	6248.00	Matches:	1200
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	4	Gaps:	0

US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)

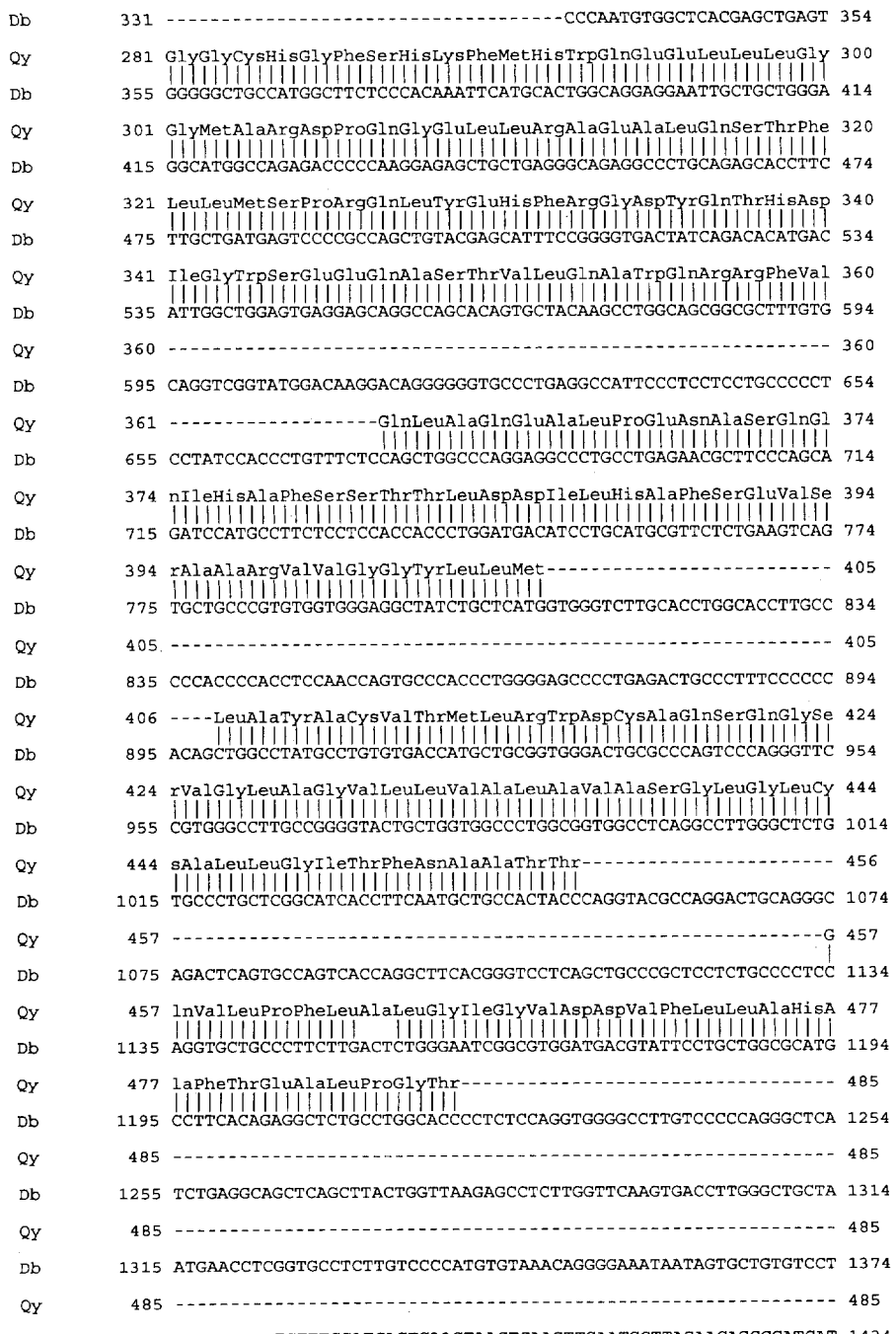
```
Qy         1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db       297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356

Qy        21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db       357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy        41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db       417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy        61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db       477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy        81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db       537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy       101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db       597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656

Qy       121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db       657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716

Qy       141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db       717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776

Qy       161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
```

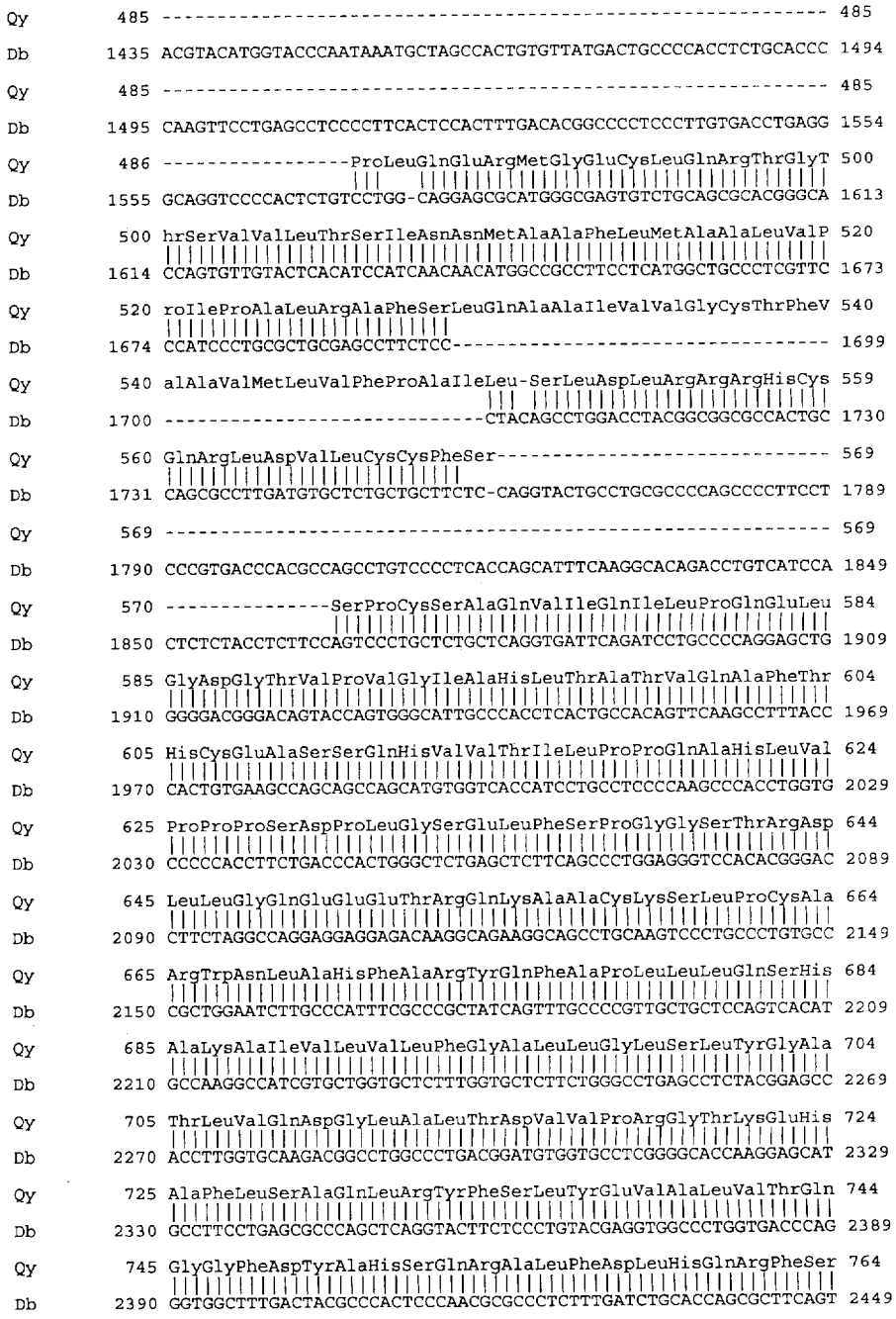

Db 777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836
Qy 181 ProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896
Qy 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956
Qy 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436
Qy 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496
Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916
Qy 541 AlaValMetLeuValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996

```
Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3897 GCCACTGGG 3905

RESULT 5
US-09-293-505-8
; Sequence 8, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
;  APPLICANT: de Sauvage, Frederic
;  APPLICANT: Carpenter, David A.
;  TITLE OF INVENTION: Patched-2
;  FILE REFERENCE: P1405R1
;  CURRENT APPLICATION NUMBER: US/09/293,505
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: US 60/081,884
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 8
;   LENGTH: 4004
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-293-505-8

Alignment Scores:
Pred. No.:                0                Length:          4004
Score:                    3955.00          Matches:         847
Percent Similarity:       65.81%           Conservative:    2
Best Local Similarity:    65.66%           Mismatches:      10
Query Match:              63.06%           Indels:          434
DB:                       3                Gaps:            10

US-09-990-046-2 (1-1203) x US-09-293-505-8 (1-4004)

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 CGGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 70

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 130

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 190

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 310

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||
Db        311 GGCTCCGCCTACCTGCCGCT---------------------------------------- 330

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240

Db        330 ---------------------------------------------------------- 330

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260

Db        330 ---------------------------------------------------------- 330

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
                                                  ||||||||||||||||||||||||
Db        331 ----------------------------------CCCAATGTGGCTCACGAGCTGAGT 354

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 594
```


Qy 360 ---------- 360
Db 595 CAGGTCGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 654
Qy 361 ----------GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGl 374
Db 655 CCTATCCACCCTGTTTCTCCAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet---------- 405
Db 775 TGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGTGGGTCTTGCACCTGGCACCTTGCC 834
Qy 405 ---------- 405
Db 835 CCCACCCCACCTCCAACCAGTGCCCACCCTGGGGAGCCCCTGAGACTGCCCTTTCCCCCC 894
Qy 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 ----------G 457
Db 1075 AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTGCTGCCCTTCTTGACTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr---------- 485
Db 1195 CCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254
Qy 485 ---------- 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 ---------- 485
Db 1315 ATGAACCTCGGTGCCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGCTGTGTCCT 1374
Qy 485 ---------- 485
Db 1375 AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 ---------- 485
Db 1435 ACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 ---------- 485
Db 1495 CAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGAGG 1554
Qy 486 ----------ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCCACTCTGTCCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTTGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTC 1673
Qy 520 roIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC---------- 1699
Qy 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys 559
Db 1700 ----------CTACAGCCTGGACCTACGGCGGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCCTGCGCCCCAGCCCCTTCCT 1789
Qy 569 ---------- 569
Db 1790 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 1849
Qy 570 ----------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------- 837
Db 2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689
Qy 837 ---------- 837

```
Db       2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749

Qy        838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809

Qy        857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869

Qy        877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2870 AACTTCTACCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929

Qy        897 LeuArg---------------------------------------------------------- 898
              ||||||
Db       2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989

Qy        898 ---------------------------------------------------------------- 898

Db       2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049

Qy        899 -------------------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
                              :::||||||||||||||||||||||||||||||||||||||||
Db       3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109

Qy        912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169

Qy        932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229

Qy        952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289

Qy        972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349

Qy        992 e---------------------------------------------------------- 992
              |
Db       3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

Qy        993 ----------------------------------------ValLeuValLeuAlaMetM 999
                                                     ||||||||||||||||||
Db       3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy        999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529

Qy       1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy       1039 lyPheLeuThrThrGlnGly 1045
                  |||   |||
Db       3590 TGAGCACGGGCACCCCGGGG 3609

RESULT 6
US-09-060-939A-8
; Sequence 8, Application US/09060939A
; Patent No. 6709838
;  GENERAL INFORMATION:
;    APPLICANT:  Frederic de Sauvage, David A. Carpenter
;    TITLE OF INVENTION:  Patched-2
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,939A
;      FILING DATE:  15-Apr-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1405
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4004 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
US-09-060-939A-8

Alignment Scores:
Pred. No.:                0                Length:          4004
Score:                    3955.00          Matches:         847
Percent Similarity:       65.81%           Conservative:    2
Best Local Similarity:    65.66%           Mismatches:      10
Query Match:              63.06%           Indels:          434
DB:                       4                Gaps:            10

US-09-990-046-2 (1-1203) x US-09-060-939A-8 (1-4004)

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 CGGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 70

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 130

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 190

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 310

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||
Db        311 GGCTCCGCCTACCTGCCGCT---------------------------------------- 330

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240

Db        330 ---------------------------------------------------------- 330

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260

Db        330 ---------------------------------------------------------- 330

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
                                                  ||||||||||||||||||||||
```


Db 331 ----------CCCAATGTGGCTCACGAGCTGAGT 354
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 355 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 594
Qy 360 ---------- 360
Db 595 CAGGTCGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 654
Qy 361 ----------GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGl 374
Db 655 CCTATCCACCCTGTTTCTCCAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet---------- 405
Db 775 TGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGTGGGTCTTGCACCTGGCACCTTGCC 834
Qy 405 ---------- 405
Db 835 CCCACCCCACCTCCAACCAGTGCCCACCCTGGGGAGCCCCTGAGACTGCCCTTTCCCCCC 894
Qy 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 ----------G 457
Db 1075 AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTGCTGCCCTTCTTGACTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr---------- 485
Db 1195 CCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254
Qy 485 ---------- 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 ---------- 485
Db 1315 ATGAACCTCGGTGCCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGCTGTGTCCT 1374
Qy 485 ---------- 485
Db 1375 AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434


Qy 485 ---------- 485
Db 1435 ACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 ---------- 485
Db 1495 CAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGAGG 1554
Qy 486 ----------ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCCACTCTGTCCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTTGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTC 1673
Qy 520 roIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC---------- 1699
Qy 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys 559
Db 1700 ----------CTACAGCCTGGACCTACGGCGGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCCTGCGCCCCAGCCCCTTCCT 1789
Qy 569 ---------- 569
Db 1790 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 1849
Qy 570 ----------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 2029
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGAGCC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTCAGT 2449

```
Qy        765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2450 TCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCACTAT 2509

Qy        785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2510 TACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569

Qy        805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2570 ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTC 2629

Qy        825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer---------------------- 837
              |||||||||||||||||||||||||||||||||||
Db       2630 ATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAG 2689

Qy        837 ---------------------------------------------------------- 837

Db       2690 GGGTCCACTAGTACAGGGGCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCT 2749

Qy        838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2750 CTGCAGCTGACCACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTC 2809

Qy        857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCC 2869

Qy        877 AsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2870 AACTTCTACCCCCCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAAC 2929

Qy        897 LeuArg------------------------------------------------------ 898
              ||||||
Db       2930 CTTCGCAGTGAGTCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCT 2989

Qy        898 ---------------------------------------------------------- 898

Db       2990 GAGCCTGAGGCCCTGCCCACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTC 3049

Qy        899 -------------------IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
                               :::||||||||||||||||||||||||||||||||||||||
Db       3050 CCTTCCCCTCCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTT 3109

Qy        912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3110 CCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGC 3169

Qy        932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3170 AGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCT 3229

Qy        952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3230 CTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCT 3289

Qy        972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3290 GGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCAT 3349

Qy        992 e---------------------------------------------------------- 992
              |
Db       3350 AGTGAGTGCTTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCAT 3409

Qy        993 ----------------------------------------ValLeuValLeuAlaMetM 999
                                                     ||||||||||||||||||||
Db       3410 CCCTCCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGA 3469

Qy        999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3470 TGACAGTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529

Qy       1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3530 TGGTGATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGG 3589

Qy       1039 lyPheLeuThrThrGlnGly 1045
                  |||   |||
Db       3590 TGAGCACGGGCACCCCGGGG 3609
```

RESULT 7
US-09-293-505-9
; Sequence 9, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 9
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-293-505-9

Alignment Scores:

Pred. No.:	1.54e-308	Length:	2082
Score:	3387.00	Matches:	656
Percent Similarity:	96.33%	Conservative:	1
Best Local Similarity:	96.19%	Mismatches:	3
Query Match:	54.00%	Indels:	23
DB:	3	Gaps:	2

US-09-990-046-2 (1-1203) x US-09-293-505-9 (1-2082)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547
```

```
Qy       181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db       548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy       201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db       608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy       221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db       668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy       241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db       728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy       261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db       788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy       281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db       848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907

Qy       301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy       321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db      1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db      1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
                                                                        ||||||||||||||||||||||||||||||||||
Db      1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
             |||||||||||||||||||||||||||||||                ||||||||
Db      1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT---------------TTCGCCCCGGAATTC 1980

Qy       681 LeuGln 682
             ||||||
Db      1981 CTGCAG 1986
```

RESULT 8
US-09-060-939A-9
; Sequence 9, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2082 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
US-09-060-939A-9

Alignment Scores:

Pred. No.:	1.54e-308	Length:	2082
Score:	3387.00	Matches:	656

Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 96.19% Mismatches: 3
Query Match: 54.00% Indels: 23
DB: 4 Gaps: 2

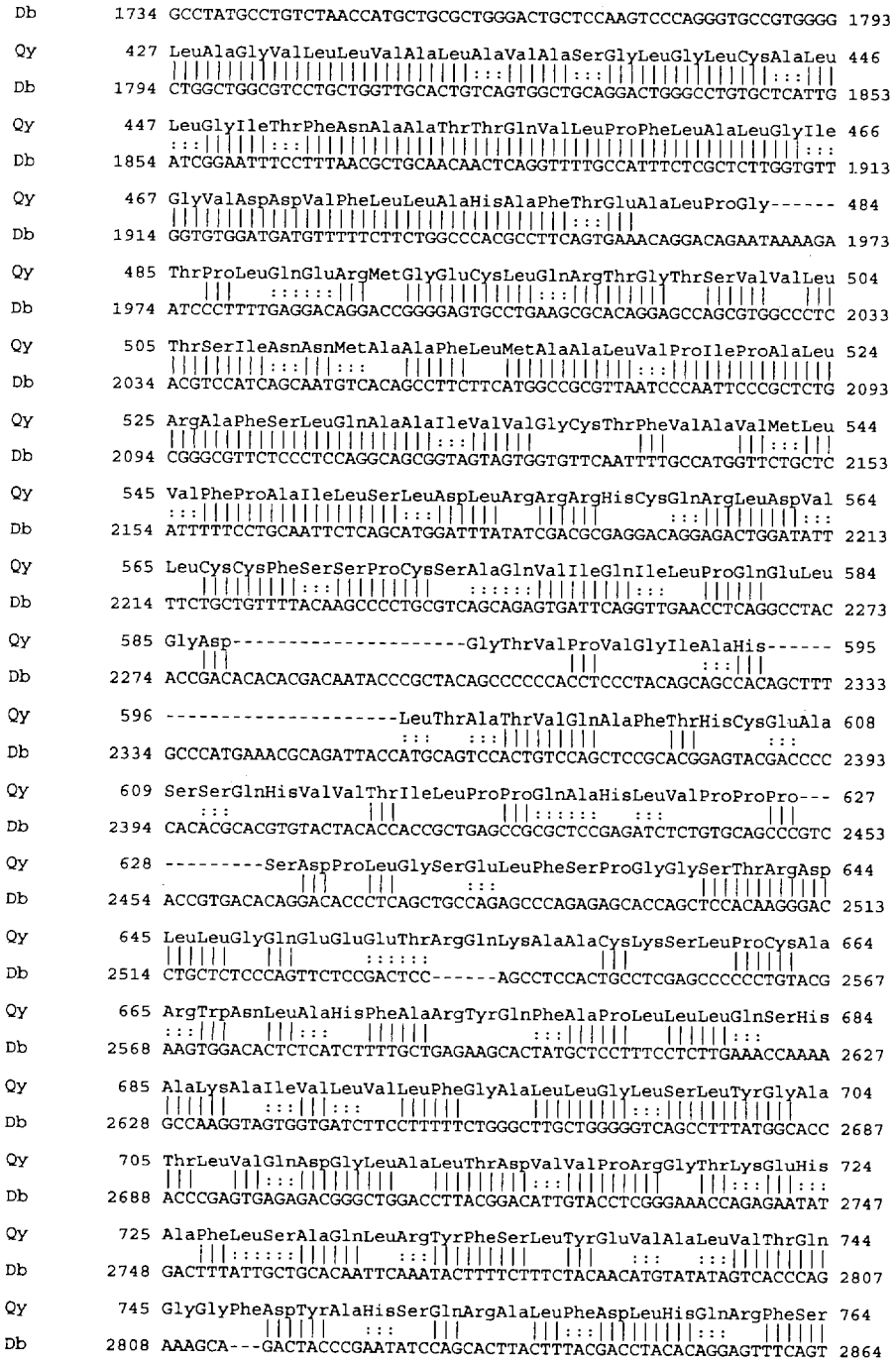
US-09-990-046-2 (1-1203) x US-09-060-939A-9 (1-2082)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 67

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 187

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 247

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 307

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 367

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 427

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 487

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 607

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 727

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 787

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 847

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 907

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 967

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        968 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1087

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1147

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 ACCACCCTGGATAACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1207

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1267

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1327

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1387

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1447

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1567

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||
Db       1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC---------------------------- 1599

Qy        541 AlaValMetLeuValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
                                              ||||||||||||||||||||||||||||||||
Db       1600 ------------------------ATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1635

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1755

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1815

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1935

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
              ||||||||||||||||||||||||||||||||                ||||||||
Db       1936 CTGCCCTGTGCCCGCTGGAATCTTGCCCAT---------------TTCGCCCCGGAATTC 1980

Qy        681 LeuGln 682
              ||||||
Db       1981 CTGCAG 1986
```

```
RESULT 9
US-08-540-406-18
; Sequence 18, Application US/08540406
; Patent No. 5837538
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/540,406
;      FILING DATE:  06-OCT-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-540-406-18

Alignment Scores:
Pred. No.:                2.75e-304      Length:          5288
Score:                    3349.00        Matches:         662
Percent Similarity:       70.02%         Conservative:    200
Best Local Similarity:    53.78%         Mismatches:      298
Query Match:              53.40%         Indels:          71
DB:                       2              Gaps:            16

US-09-990-046-2 (1-1203) x US-08-540-406-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
              |||||||||        |||       |||       ||||||      |||
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
                   ||||||||||||||||||||||||    ||||||   |||||||||   ||||||
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
              |||   ||||||::::::|||||||||    |||   :::||||||||   |||||||||
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
                 |||:::||||||:::   |||   :::|||||||||:::|||:::||||||||||||
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
              ||||||   |||||||||:::|||||||:::||||||::::::|||:::||||||||||||
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
                 :::      |||::::::|||||||||   ::::::||||||   |||:::|||||||
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
              |||||||||        ||||||   :::||||||   ||||||:::|||   |||
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
                 :::|||   :::   |||   |||       :::|||||||||||||||       :::
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
              |||   |||   ::::::   :::|||||||   |||:::|||||||:::|||:::|||||
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
              ||||||||||||||||||||||||||||||||||   |||:::||||||||||   |||:::
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
              |||   ::::::||||||||   ||||||   :::   ||||||||||||
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
                    ::::::   :::   |||:::|||:::||||||:::||||||       |||
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
              :::   ||||||||||||:::|||   |||       ||||||   :::|||||||||
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
              :::|||   :::      ::::::|||      |||:::|||||||||||||||   |||
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
              |||:::|||||||||||||||||||||:::::|||||      ::::::
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
              |||:::|||:::   |||   |||||||||:::   |||   ||||||:::|||:::|||
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
              :::|||||||||||||:::|||   :::|||   :::|||   |||   |||:::|||:::
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
              :::|||:::   :::|||:::||||||||||||   :::|||:::::      ::::::
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
              :::   :::|||::::::|||:::::::   :::|||:::::::|||||||||||||||||
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
              |||   :::||||||:::||||||      ||||||      |||||||||||||||||
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
              ||||||||||:::|||||||||||||||||||||:::::|||||||:::||||||
Db       1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793

Qy        427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
              ||||||||||||||||||||||||||:::||||||:::|||||||||||||||:::|||
Db       1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853

Qy        447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
              :::|||||||:::|||||||||||||||||||||||||||||||||||||||||||:::
Db       1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913

Qy        467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
```

```
Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
                                     |||                               |||  ::
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
                :     |||   |||     |||   |||
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173

RESULT 10
US-08-656-055-18
; Sequence 18, Application US/08656055
; Patent No. 6027882
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,055
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/540,406
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-656-055-18

Alignment Scores:
Pred. No.:              2.75e-304      Length:          5288
Score:                  3349.00        Matches:         662
Percent Similarity:     70.02%         Conservative:    200
Best Local Similarity:  53.78%         Mismatches:      298
Query Match:            53.40%         Indels:          71
DB:                     3              Gaps:            16

US-09-990-046-2 (1-1203) x US-08-656-055-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
              |||||||||       |||     |||      ||||||      |||
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
                   ||||||||||||||||||||||||   ||||||   |||||||||   ||||||
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
                |||   ||||||::::::|||||||||   |||   :::|||||||||   |||||||||
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
              |||:::|||||:::   |||   :::|||||||||:::|||:::|||||||||||||||
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
              ||||||   |||||||||:::|||||:::|||||:::::::|||:::|||||||||||||
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
                 :::     |||:::::||||||||   ::::::|||||   |||:::||||||
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
              |||||||||       ||||||   :::|||||||   ||||||:::|||   |||
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
                 :::|||   :::   |||   |||       :::|||||||||||||||||       :::
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrPro 188
              |||   |||   ::::::   :::||||||   |||:::||||||:::|||:::||||||
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
              ||||||||||||||||||||||||||||||||||||||||   |||:::|||||||||   |||:::
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
              |||   ::::::||||||||   ||||||   :::   ||||||||||||
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
                    ::::::   :::   |||:::|||:::||||||:::||||||       |||
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
              :::   ||||||||||||:::|||   |||       ||||||   :::||||||||||
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
              :::|||   :::       ::::::|||       |||:::||||||||||||||||   |||
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
                 |||:::|||||||||||||||||||||||:::::||||||       ::::::
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
              |||:::|||:::   |||   |||||||||:::   |||   ||||||:::|||:::|||
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
              :::||||||||||||:::|||   :::|||   :::|||   |||   |||:::|||:::
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
              :::|||:::   :::|||:::||||||||||||   :::|||::::::       ::::::
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
              :::   :::|||:::::|||::::::   :::|||:::::|||||||||||||||||||
Db       1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673

Qy        387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
              |||   :::||||||:::|||||||       ||||||       |||||||||||||||||
Db       1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733

Qy        407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
              ||||||||||||:::|||||||||||||||||||||||:::::||||||||||:::||||||
```


Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp--------------------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 --------------------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
Qy 944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464
Qy 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524
Qy 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584
Qy 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db 3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644
Qy 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db 3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704
Qy 1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db 3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764
Qy 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db 3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824
Qy 1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db 3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884
Qy 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

```
Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG----------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

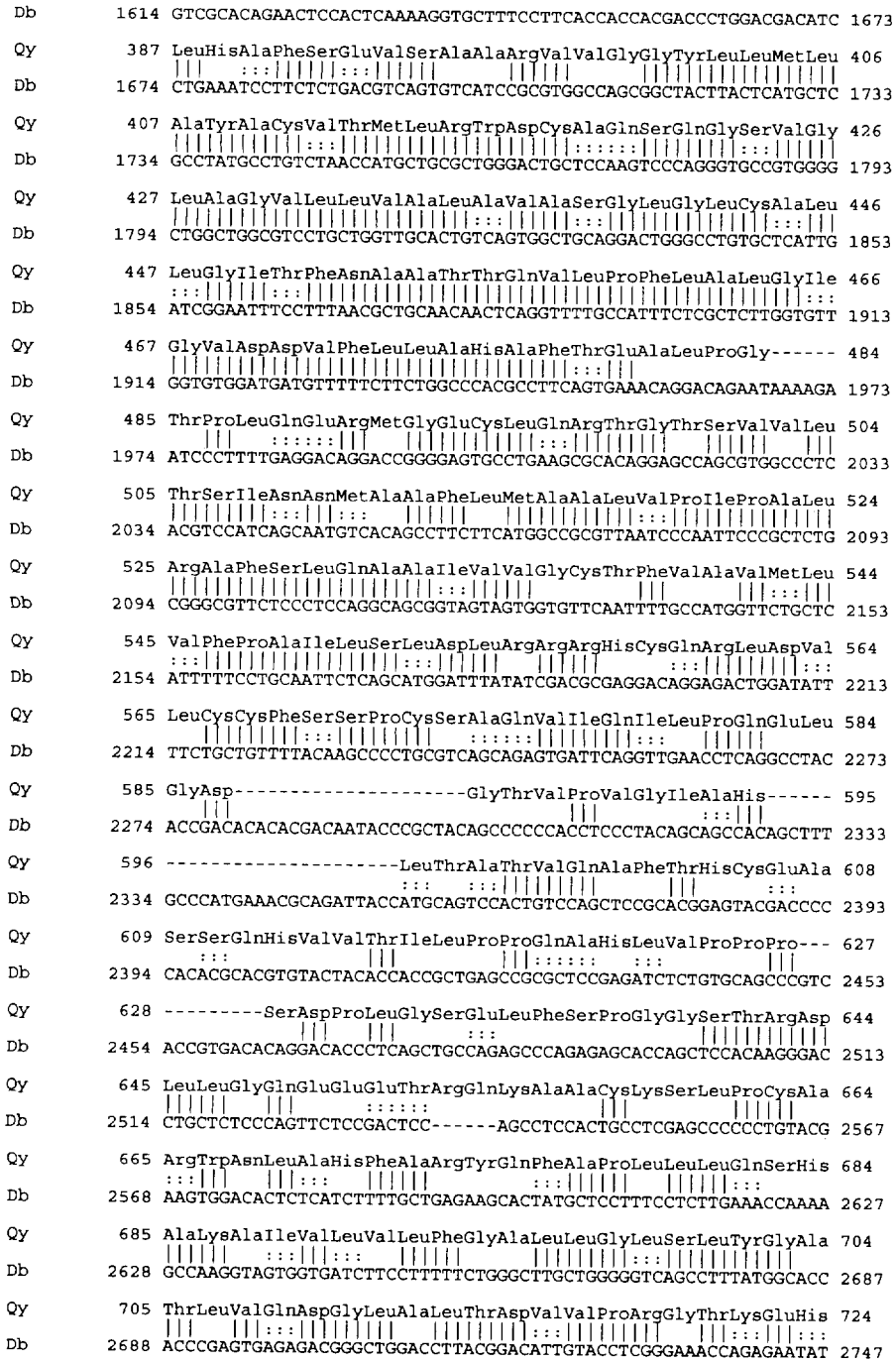
RESULT 11
US-08-954-668-18
; Sequence 18, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-954-668-18

Alignment Scores:

Pred. No.:	2.75e-304	Length:	5288
Score:	3349.00	Matches:	662
Percent Similarity:	70.02%	Conservative:	200
Best Local Similarity:	53.78%	Mismatches:	298
Query Match:	53.40%	Indels:	71
DB:	3	Gaps:	16

US-09-990-046-2 (1-1203) x US-08-954-668-18 (1-5288)

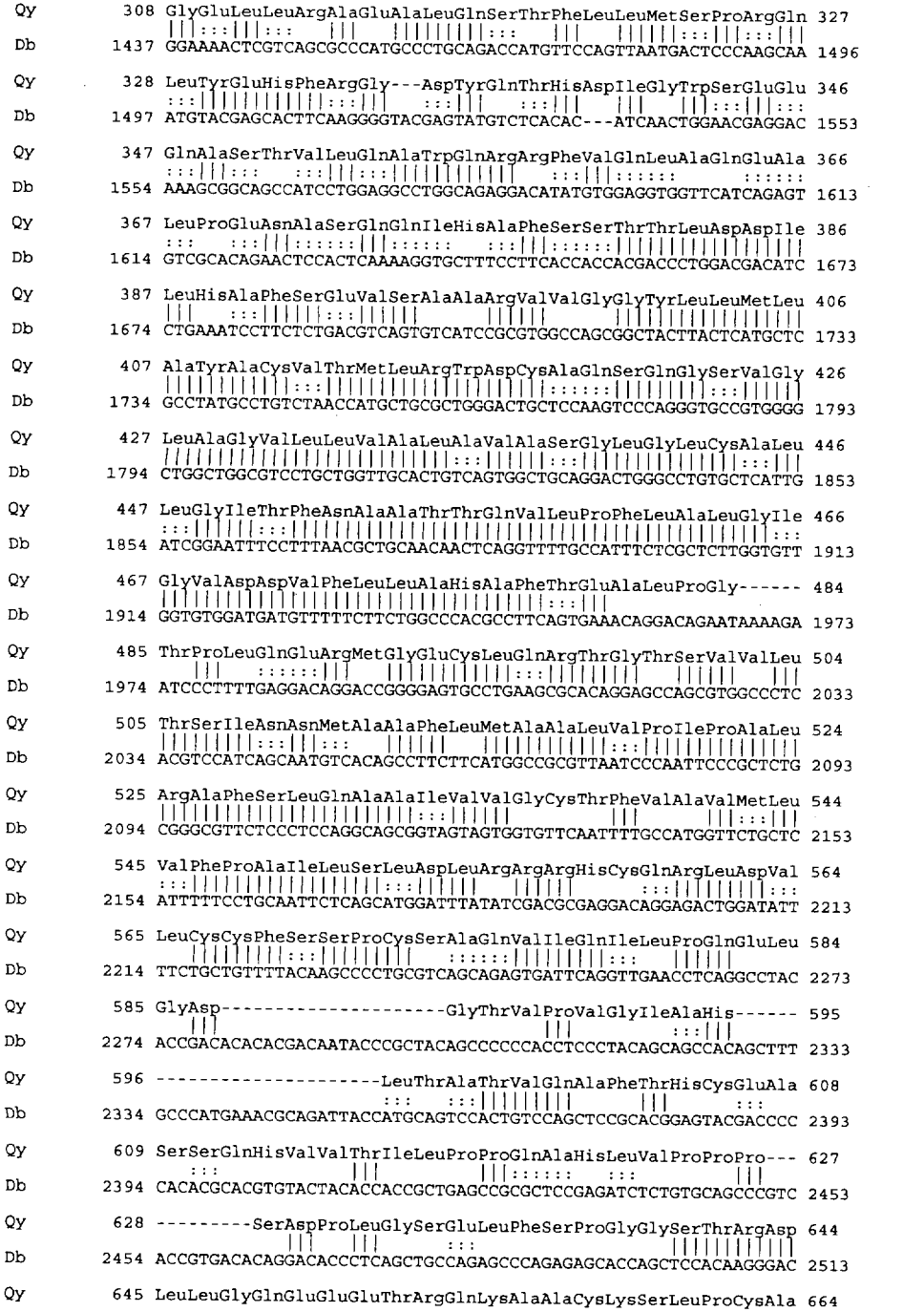
```
Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30

Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuGluGlyGlyMetAlaArgAspProGln 307
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436

Qy        308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db       1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496

Qy        328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db       1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553

Qy        347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db       1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613

Qy        367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
```


Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673
Qy 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733
Qy 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
Qy 944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464
Qy 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524
Qy 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584
Qy 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db 3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644
Qy 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db 3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704
Qy 1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db 3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764
Qy 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db 3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

```
Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG------------ 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

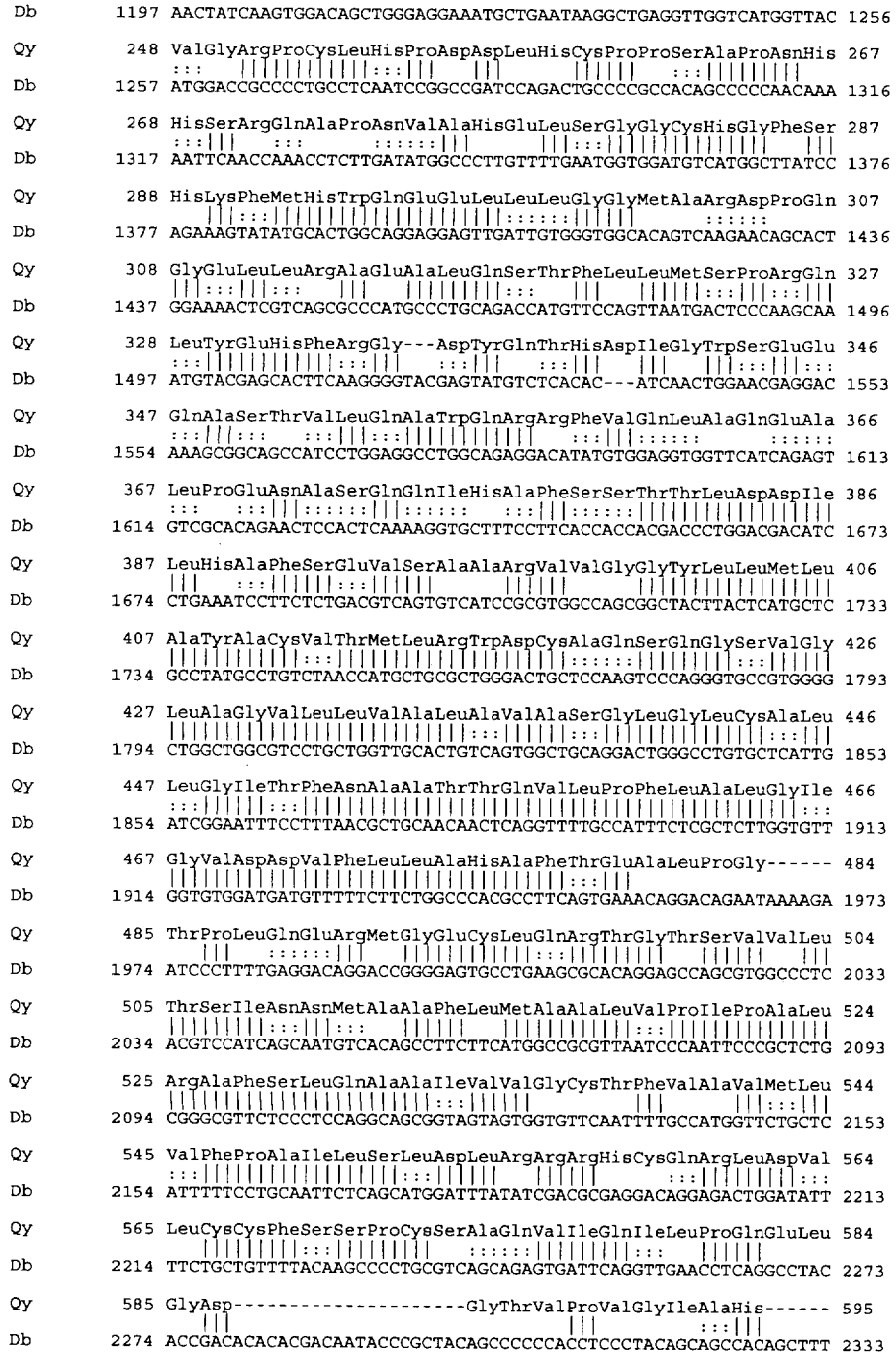
```
RESULT 12
US-08-918-658-18
; Sequence 18, Application US/08918658
; Patent No. 6429354
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/918,658
;             FILING DATE: 22-Aug-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/656,055
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/540,406
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5288 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
```

```
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-918-658-18

Alignment Scores:
Pred. No.:              2.75e-304       Length:          5288
Score:                  3349.00         Matches:         662
Percent Similarity:     70.02%          Conservative:    200
Best Local Similarity:  53.78%          Mismatches:      298
Query Match:            53.40%          Indels:          71
DB:                     4               Gaps:            16

US-09-990-046-2 (1-1203) x US-08-918-658-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db       1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256

Qy        248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db       1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316

Qy        268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db       1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376

Qy        288 HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln 307
Db       1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436
```

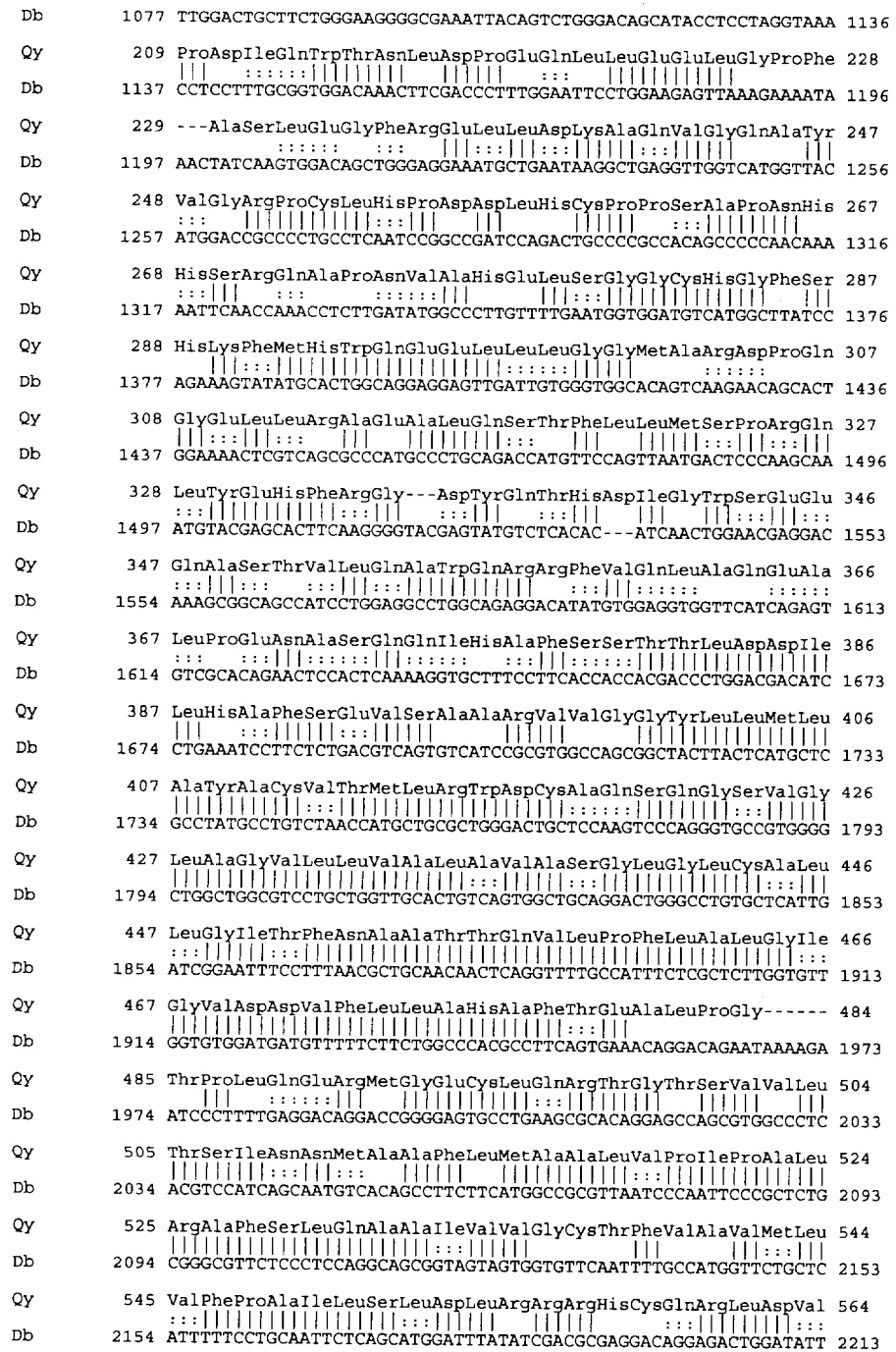

Qy 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496
Qy 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553
Qy 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613
Qy 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673
Qy 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733
Qy 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
Qy 944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464
Qy 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524
Qy 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584
Qy 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023

```
Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
                |||   :::|||   ||||||     ||||||||||||   ||||||||||||
Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
              |||||||||:::|||||||||||||||:::||||||||||||||||||   |||||||||
Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
              ||||||||||||||||||||    |||   :::||||||:::||||||:::|||:::|||
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
              ||||||||||||||||||||||||||||      ||||||   |||||||||  :::|||
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
                              |||   :::      |||||||||
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG----------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
              |||  ||||||          |||                                  ::
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG---------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
              :  |||      :::   ||||||
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
                                    |||                              |||   ::
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
              :      |||   |||      |||   |||
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

```
RESULT 13
US-09-724-631-18
; Sequence 18, Application US/09724631
; Patent No. 6551782
;   GENERAL INFORMATION:
;        APPLICANT: SCOTT, MATHEW P
;                   GOODRICH, LISA V
;                   JOHNSON, RONALD L
;        TITLE OF INVENTION: Patched Genes and their Use
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/724,631
;             FILING DATE: 28-No. 6551782-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/656,055
;             FILING DATE: 1996-05-31
;             APPLICATION NUMBER: 08/540,406
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rowland, Bertram I
;             REGISTRATION NUMBER: 20015
;             REFERENCE/DOCKET NUMBER: a60190-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5288 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-724-631-18

Alignment Scores:
Pred. No.:                2.75e-304      Length:          5288
Score:                    3349.00        Matches:         662
Percent Similarity:       70.02%         Conservative:    200
Best Local Similarity:    53.78%         Mismatches:      298
Query Match:              53.40%         Indels:          71
DB:                       4              Gaps:            16

US-09-990-046-2 (1-1203) x US-09-724-631-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
              |||||||||          |||       |||       ||||||      |||
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
                   ||||||||||||||||||||||||   ||||||   |||||||||   ||||||
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
              |||   ||||||::::::|||||||||   |||   :::|||||||||   |||||||||
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
              |||:::||||||:::   |||   :::|||||||||:::|||:::||||||||||||
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
              ||||||   |||||||||:::||||||:::||||||::::::|||:::||||||||||||
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
                 :::      |||::::::|||||||||   ::::::||||||   |||:::||||||
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
              |||||||||       ||||||   :::|||||||   |||||||:::|||   |||
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
              :::|||  :::   |||   |||      :::||||||||||||||||      :::
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProProCysValIleLeuThrPro 188
              |||   |||   ::::::   :::||||||   |||:::||||||:::|||:::||||||
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
              ||||||||||||||||||||||||||||||||||||   |||:::||||||||   |||:::
Db       1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136

Qy        209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
              |||   ::::::||||||||   ||||||   :::   ||||||||||||
Db       1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196

Qy        229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
                    ::::::   :::   |||:::|||:::|||||||:::|||||||       |||
```


Db 1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256
Qy 248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316
Qy 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376
Qy 288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436
Qy 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496
Qy 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553
Qy 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613
Qy 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673
Qy 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733
Qy 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284
Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344
Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404

```
Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db       3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464

Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db       3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524

Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db       3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584

Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG----------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173

RESULT 14
US-08-954-701A-18
; Sequence 18, Application US/08954701A
; Patent No. 6610507
;  GENERAL INFORMATION:
;    APPLICANT:  SCOTT, MATHEW P
;    APPLICANT:  GOODRICH, LISA V
;    APPLICANT:  JOHNSON, RONALD L
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,701A
;      FILING DATE:  20-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36709
;      REFERENCE/DOCKET NUMBER:  SUV-003.08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-954-701A-18

Alignment Scores:
Pred. No.:                2.75e-304      Length:          5288
Score:                    3349.00        Matches:         662
Percent Similarity:       70.02%         Conservative:    200
Best Local Similarity:    53.78%         Mismatches:      298
Query Match:              53.40%         Indels:          71
DB:                       4              Gaps:            16

US-09-990-046-2 (1-1203) x US-08-954-701A-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuProCysValIleLeuThrPro 188
Db       1017 GAAACAGGTTACATGGATCAGATAATAGAATATCTTTACCCTTGTTTGATTATTACACCT 1076

Qy        189 LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
```


Db 1077 TTGGACTGCTTCTGGGAAGGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAA 1136
Qy 209 ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeuGlyProPhe 228
Db 1137 CCTCCTTTGCGGTGGACAAACTTCGACCCTTTGGAATTCCTGGAAGAGTTAAAGAAAATA 1196
Qy 229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
Db 1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTTGGTCATGGTTAC 1256
Qy 248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGGACCGCCCCTGCCTCAATCCGGCCGATCCAGACTGCCCCGCCACAGCCCCCAACAAA 1316
Qy 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAAACCTCTTGATATGGCCCTTGTTTTGAATGGTGGATGTCATGGCTTATCC 1376
Qy 288 HisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGTGGGTGGCACAGTCAAGAACAGCACT 1436
Qy 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAAAACTCGTCAGCGCCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496
Qy 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC---ATCAACTGGAACGAGGAC 1553
Qy 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAAGCGGCAGCCATCCTGGAGGCCTGGCAGAGGACATATGTGGAGGTGGTTCATCAGAGT 1613
Qy 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTCACCACCACGACCCTGGACGACATC 1673
Qy 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTTCTCTGACGTCAGTGTCATCCGCGTGGCCAGCGGCTACTTACTCATGCTC 1733
Qy 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCCTGTCTAACCATGCTGCGCTGGGACTGCTCCAAGTCCCAGGGTGCCGTGGGG 1793
Qy 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCCTGCTGGTTGCACTGTCAGTGGCTGCAGGACTGGGCCTGTGCTCATTG 1853
Qy 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTTCCTTTAACGCTGCAACAACTCAGGTTTTGCCATTTCTCGCTCTTGGTGTT 1913
Qy 467 GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly------ 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCACGCCTTCAGTGAAACAGGACAGAATAAAAGA 1973
Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCCAGCGTGGCCCTC 2033
Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTCCCGCTCTG 2093
Qy 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCTCCCTCCAGGCAGCGGTAGTAGTGGTGTTCAATTTTGCCATGGTTCTGCTC 2153
Qy 545 ValProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTTCCTGCAATTCTCAGCATGGATTTATATCGACGCGAGGACAGGAGACTGGATATT 2213
Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTACAAGCCCCTGCGTCAGCAGAGTGATTCAGGTTGAACCTCAGGCCTAC 2273
Qy 585 GlyAsp----------GlyThrValProValGlyIleAlaHis------ 595
Db 2274 ACCGACACACACGACAATACCCGCTACAGCCCCCCACCTCCCTACAGCAGCCACAGCTTT 2333
Qy 596 ----------LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAACGCAGATTACCATGCAGTCCACTGTCCAGCTCCGCACGGAGTACGACCCC 2393
Qy 609 SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProProPro--- 627
Db 2394 CACACGCACGTGTACTACACCACCGCTGAGCCGCGCTCCGAGATCTCTGTGCAGCCCGTC 2453
Qy 628 ---------SerAspProLeuGlySerGluLeuPheSerProGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCTCAGCTGCCAGAGCCCAGAGAGCACCAGCTCCACAAGGGAC 2513
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCCAGTTCTCCGACTCC------AGCCTCCACTGCCTCGAGCCCCCCTGTACG 2567
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGCTGAGAAGCACTATGCTCCTTTCCTCTTGAAACCAAAA 2627
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGGTGATCTTCCTTTTTCTGGGCTTGCTGGGGGTCAGCCTTTATGGCACC 2687
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACCTCGGGAAACCAGAGAATAT 2747
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAATTCAAATACTTTTCTTTCTACAACATGTATATAGTCACCCAG 2807
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
Qy 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCACTAC 2924
Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGGACTTCAGGATGCATTTGACAGTGACTGGGAAACCGGGAAA 2984
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAATTACAAGAATGGATCAGACGATGGAGTCCTTGCCTACAAACTCCTG 3044
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAACCGGCAGCCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATGCAGATGGCATCATTAATCCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC 3164
Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGlu 884
Db 3165 AGCAACGACCCCGTCGCGTATGCTGCCTCCCAGGCCAACATCCGGCCACACCGACCAGAA 3224
Qy 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db 3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284

```
Qy        904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db       3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344

Qy        924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db       3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404

Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db       3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464

Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db       3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524

Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db       3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584

Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG----------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173

RESULT 15
PCT-US95-13233-18
; Sequence 18, Application PC/TUS9513233
;  GENERAL INFORMATION:
;    APPLICANT:  THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY
;    TITLE OF INVENTION:  Patched Genes and their Use
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13233
;      FILING DATE:  06-OCT-1990
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  a60190-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-13233-18

Alignment Scores:
Pred. No.:                2.75e-304      Length:          5288
Score:                    3349.00        Matches:         662
Percent Similarity:       70.02%         Conservative:    200
Best Local Similarity:    53.78%         Mismatches:      298
Query Match:              53.40%         Indels:          71
DB:                       5              Gaps:            16

US-09-990-046-2 (1-1203) x PCT-US95-13233-18 (1-5288)

Qy         12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
Db        540 CCCAGCTACTGC---GACGCCGCCTTCGCTCTGGAGCAGATTTCCAAGGGGAAGGCTACT 596

Qy         31 ------LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db        597 GGCCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAACTGGGT 656

Qy         49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla 68
Db        657 TGTTACATTCAAAAAAACTGCGGCAAGTTCTTGGTTGTGGGCCTCCTCATATTTGGGGCC 716

Qy         69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db        717 TTCGCGGTGGGATTAAAAGCAGCGAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA 776

Qy         89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLysLeuGlyGluGluAla 108
Db        777 GTTGGAGGACGAGTAAGTCGTGAATTAAATTATACTCGCCAGAAGATTGGAGAAGAGGCT 836

Qy        109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
Db        837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGGTGCTAATGTCCTGACC 896

Qy        129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db        897 ACAGAAGCGCTCCTACAACACCTGGACTCGGCACTCCAGGCCAGCCGTGTCCATGTATAC 956

Qy        149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db        957 ATGTACAACAGGCAGTGGAAATTGGAACATTTGTGTTACAAATCAGGAGAGCTTATCACA 1016

Qy        169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrPro 188
```

```
Qy        885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
              |||:::|||||||||   |||         |||      ||||||||||||   |||:::
Db       3225 TGGGTCCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG 3284

Qy        904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
              |||:::|||:::|||||||||||||||||   |||   ||||||:::   |||:::||||||
Db       3285 CCCATCGAGTATGCCCAGTTCCCTTTCTACCTCAACGGGTTGCGGGACACCTCAGACTTT 3344

Qy        924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
              ||||||||||||||||   |||       |||:::                 |||:::
Db       3345 GTGGAGGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404

Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
              :::||||||:::|||   ||||||||||||||||||||||||:::|||||||||
Db       3405 AGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCAGTACATCGGCCTCCGCCACTGG 3464

Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
                 ||||||   :::   ::::::|||   ||||||||||||||||||||:::   |||
Db       3465 CTGCTGCTGTTCATCAGCGTGGTGTTGGCCTGCACATTCCTCGTGTGCGCTGTCTTCCTT 3524

Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
              ||||||||||||||||||||:::||||||:::||||||||:::|||||||||||||||||
Db       3525 CTGAACCCCTGGACGGCCGGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTG 3584

Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
              ||||||:::||||||   :::||||||||||||||||||:::|||||||||||||||:::
Db       3585 TTCGGCATGATGGGCCTCATCGGAATCAAGCTCAGTGCCGTGCCCGTGGTCATCCTGATC 3644

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
              ||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTCACGTTGCTTTGGCCTTTCTGACGGCC 3704

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
                 |||   :::|||   ||||||       ||||||||||||   ||||||||||||
Db       3705 ATCGGCGACAAGAACCGCAGGGCTGTGCTTGCCCTGGAGCACATGTTTGCACCCGTCCTG 3764

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
              ||||||||:::||||||||||||||||:::||||||||||||||||||   |||||||||
Db       3765 GATGGCGCCGTGTCCACTCTGCTGGGAGTGCTGATGCTGGCGGGATCTGAGTTCGACTTC 3824

Qy       1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
              ||||||||||||||||||||   |||   :::||||||:::||||||:::|||:::|||
Db       3825 ATTGTCAGGTATTTCTTTGCTGTGCTGGCGATCCTCACCATCCTCGGCGTTCTCAATGGG 3884

Qy       1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
              ||||||||||||||||||||||||||||||       ||||||   |||||||| :::|||
Db       3885 CTGGTTTTGCTTCCCGTGCTTTTGTCTTTCTTTGGACCATATCCTGAGGTGTCTCCAGCC 3944

Qy       1123 tTyrLys------------GluSerProGluIleLeuSerProProAlaProGlnGlyGl 1139
                               |||   :::      |||||||||
Db       3945 AACGGCTTGAACCGCCTGCCCACACCCTCCCCTGAGCCACCCCCCAGCG----------- 3993

Qy       1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
                    |||   ||||||          |||                          ::
Db       3994 ----------TGGTCCGCTTCGCCATGCCGCCCG--------------------GCCAC 4022

Qy       1159 rMetThrValAlaIleHisProPro---------------------------------- 1167
              :   |||       :::   ||||||
Db       4023 ACGCACAGCGGGTCTGATTCCTCCGACTCGGAGTATAGTTCCCAGACGACAGTGTCAGGC 4082

Qy       1168 ----------------------ProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
                                     |||                          |||   ::
Db       4083 CTCAGCGAGGAGCTTCGGCACTACGAGGCCCAGCAGGGCGCGGGAGGCCCTGCCCACCAA 4142

Qy       1180 uProProTrpSerProAlaAlaThrSerSer 1190
              :      |||   |||       |||   |||
Db       4143 GTGATCGTGGAAGCCACAGAAAACCCCGTCT 4173
```

Search completed: November 22, 2004, 12:11:09
Job time : 336 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:50 ; Search time 7917 Seconds
(without alignments)
7185.741 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09990046/runat_21112004_130919_18532/app_query.fasta_1.1351
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990046_@CGN_1_1_4879_@runat_21112004_130919_18532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	3612	9	AF091501	AF091501 Homo sapi
2	6272	100.0	3641	9	AY358555	AY358555 Homo sapi
3	6272	100.0	3765	9	AY359016	AY359016 Homo sapi
4	6272	100.0	4030	6	BD194644	BD194644 Vertebrat
5	6272	100.0	4030	6	AR194379	AR194379 Sequence
6	6272	100.0	4030	6	AR489133	AR489133 Sequence
7	6248	99.6	4391	6	AR175919	AR175919 Sequence
8	6248	99.6	4391	6	AR374936	AR374936 Sequence
9	6229	99.3	3612	9	AF087651	AF087651 Homo sapi
10	5911	94.2	3453	6	BD227641	BD227641 Novel con
11	5911	94.2	3453	9	AF119569	AF119569 Homo sapi
12	5599	89.3	3549	10	AB010833	AB010833 Mus muscu
13	5589.5	89.1	4402	10	BC058397	BC058397 Mus muscu
14	5490	87.5	3195	6	CQ717145	CQ717145 Sequence
15	4682.5	74.7	12886	6	BD227644	BD227644 Novel con
16	4233.5	67.5	23118	9	AY438664	AY438664 Homo sapi
17	4119.5	65.7	4762	5	AB037688	AB037688 Xenopus l
18	4106.5	65.5	4528	5	BC070995	BC070995 Xenopus l
19	4042.5	64.5	3672	5	DRPATCH	X98883 D.rerio mRN
20	3991.5	63.6	170141	2	AL611928	AL611928 Homo sapi
c 21	3975	63.4	171656	9	AL136380	AL136380 Human DNA
22	3955	63.1	4004	6	BD194648	BD194648 Vertebrat
23	3955	63.1	4004	6	AR194383	AR194383 Sequence
24	3955	63.1	4004	6	AR489137	AR489137 Sequence
25	3674.5	58.6	134412	10	AC124037	AC124037 Mus Muscu
c 26	3674.5	58.6	230447	10	AL671866	AL671866 Mouse DNA
27	3387	54.0	2082	6	BD194649	BD194649 Vertebrat
28	3387	54.0	2082	6	AR194384	AR194384 Sequence
29	3387	54.0	2082	6	AR489138	AR489138 Sequence
30	3356	53.5	4305	10	AY357891	AY357891 Rattus no
31	3349	53.4	4344	6	CQ725013	CQ725013 Sequence
32	3349	53.4	4344	9	HSU59464	U59464 Human PATCH
33	3349	53.4	5288	6	AR055796	AR055796 Sequence
34	3349	53.4	5288	6	AR124819	AR124819 Sequence
35	3349	53.4	5288	6	AR222516	AR222516 Sequence
36	3349	53.4	5288	6	AR307508	AR307508 Sequence
37	3349	53.4	5288	6	AR382414	AR382414 Sequence
38	3345	53.3	2748	5	AF409095	AF409095 Gallus ga
39	3340	53.3	4502	5	GGU40074	U40074 Gallus gall
40	3337	53.2	4305	10	MMU46155	U46155 Mus musculu
41	3337	53.2	5187	6	AR055788	AR055788 Sequence
42	3337	53.2	5187	6	AR055791	AR055791 Sequence
43	3337	53.2	5187	6	AR124811	AR124811 Sequence
44	3337	53.2	5187	6	AR124814	AR124814 Sequence
45	3337	53.2	5187	6	AR222508	AR222508 Sequence

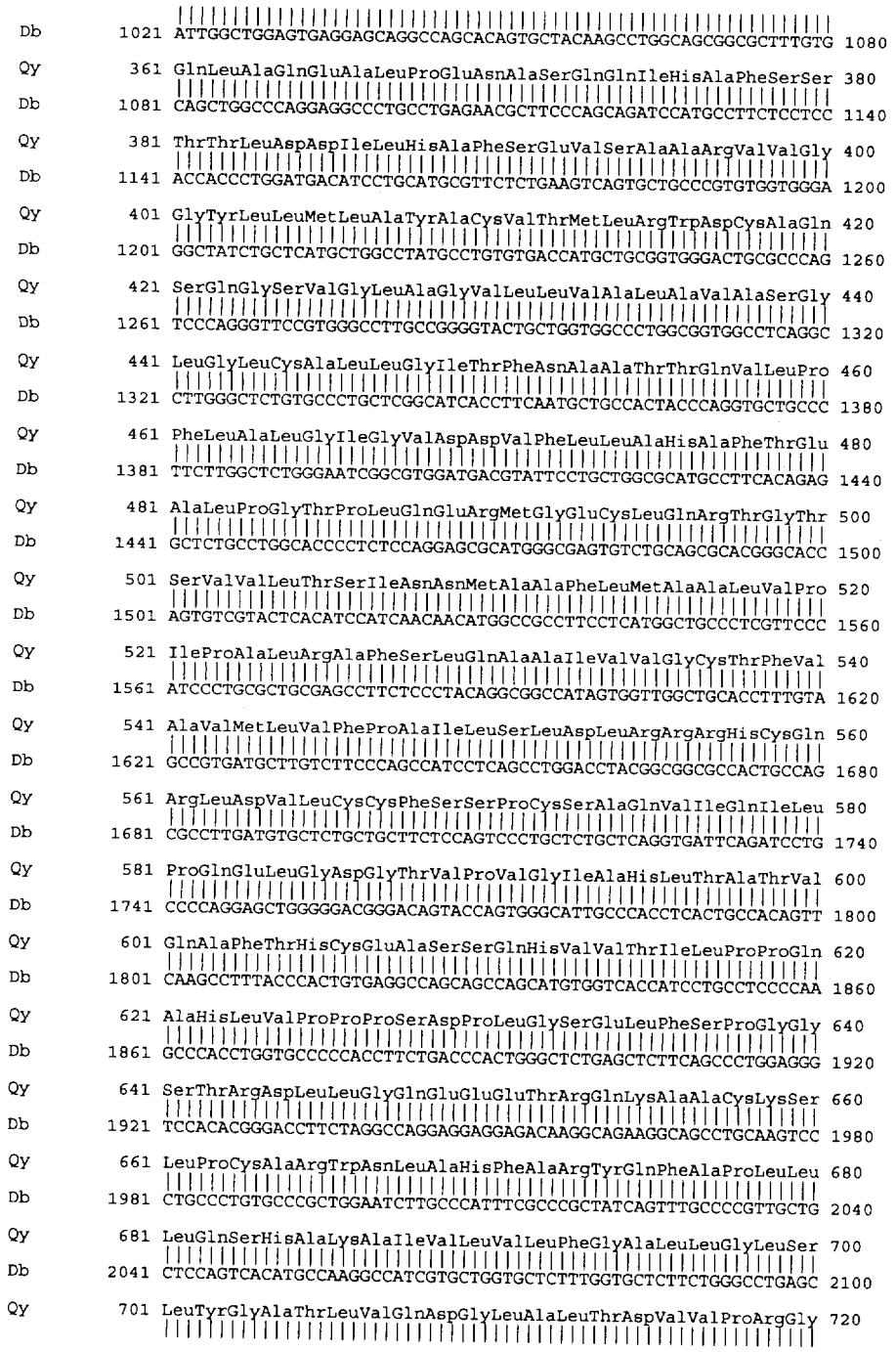
ALIGNMENTS

RESULT 1
AF091501
LOCUS AF091501 3612 bp mRNA linear PRI 30-NOV-1998
DEFINITION Homo sapiens receptor protein patched 2 (PTCH2) mRNA, complete cds.
ACCESSION AF091501
VERSION AF091501.1 GI:3929234
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3612)
AUTHORS Carpenter,D., Stone,D.M., Brush,J., Ryan,A., Armanini,M., Frantz,G., Rosenthal,A. and de Sauvage,F.J.
TITLE Characterization of two patched receptors for the vertebrate hedgehog protein family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13630-13634 (1998)
MEDLINE 99030620
PUBMED 9811851
REFERENCE 2 (bases 1 to 3612)
AUTHORS de Sauvage,F.J. and Carpenter,D.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1998) Molecular Oncology, Genentech Inc, 1 DNA Way, So. San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
source 1. .3612
/organism="Homo sapiens"
/mol_type="mRNA"

```
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p32-p36"
     gene            1. .3612
                     /gene="PTCH2"
     CDS             1. .3612
                     /gene="PTCH2"
                     /note="12 TM receptor protein; Hedgehog receptor"
                     /codon_start=1
                     /product="receptor protein patched 2"
                     /protein_id="AAC79847.1"
                     /db_xref="GI:3929235"
                     /translation="MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLL
                     FSLGCGIQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKE
                     KLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKIC
                     YKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
                     EQLLEELGPFASLEGFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVA
                     HELSGGCHGFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG
                     DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSE
                     VSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
                     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSIN
                     NMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLC
                     CFSSPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLV
                     PPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQ
                     SHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
                     LVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQ
                     DWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELF
                     YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLL
                     RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
                     VCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGV
                     EFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF
                     FAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGAS
                     SSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGPATG"
ORIGIN

Alignment Scores:
Pred. No.:                0                Length:          3612
Score:                    6272.00          Matches:         1203
Percent Similarity:       100.00%          Conservative:    0
Best Local Similarity:    100.00%          Mismatches:      0
Query Match:              100.00%          Indels:          0
DB:                       9                Gaps:            0

US-09-990-046-2 (1-1203) x AF091501 (1-3612)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 60

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 120

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 180

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 240

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 300

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 360

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 420

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 480

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 540

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 600

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 660

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 720

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 780

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 840

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 900

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 960

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1020

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1080

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1140

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1200

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1260

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1320

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1380

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1440

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1500

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
```

```
Db      1501 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1560
Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1561 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1620
Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1621 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1680
Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1681 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1740
Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1741 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1800
Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1801 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1860
Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1861 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1920
Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1921 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1980
Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1981 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2040
Qy       681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db      2041 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2100
Qy       701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db      2101 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2160
Qy       721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db      2161 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2220
Qy       741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db      2221 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2280
Qy       761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db      2281 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2340
Qy       781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db      2341 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2400
Qy       801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db      2401 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2460
Qy       821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db      2461 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2520
Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2521 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2580
Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2581 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2640
Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db      2641 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2700
Qy       901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2701 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2760
Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2761 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2820
Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      2821 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2880
Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      2881 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2940
Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      2941 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3000
Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3001 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3060
Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3061 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3120
Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3121 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3180
Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3181 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3240
Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3241 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3300
Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3301 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3360
Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3361 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3420
Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3421 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3480
Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3481 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3540
Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3541 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3600
Qy      1201 AlaThrGly 1203
Db      3601 GCCACTGGG 3609

RESULT 2
AY358555
LOCUS       AY358555                3641 bp    mRNA    linear   PRI 03-OCT-2003
```

```
DEFINITION  Homo sapiens clone DNA35621 Patched 2 (UNQ560) mRNA, complete cds.
ACCESSION   AY358555
VERSION     AY358555.1  GI:37182232
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3641)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 3641)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .3641
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA35621"
     gene            1. .3641
                     /locus_tag="UNQ560"
     CDS             1. .3636
                     /locus_tag="UNQ560"
                     /note="PRO1121"
                     /codon_start=1
                     /product="Patched 2"
                     /protein_id="AAQ88919.1"
                     /db_xref="GI:37182233"
                     /translation="MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLL
                     FSLGCGIQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKE
                     KLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKIC
                     YKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
                     EQLLEELGPFASLEGFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVA
                     HELSGGCHGFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG
                     DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSE
                     VSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
                     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSIN
                     NMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLC
                     CFSSPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLV
                     PPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQ
                     SHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
                     LVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQ
                     DWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELF
                     YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLL
                     RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
                     VCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGV
                     EFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF
                     FAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGAS
                     SSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGPATGD
                     YKDDDDK"
ORIGIN

Alignment Scores:
Pred. No.:                0          Length:          3641
Score:                    6272.00    Matches:         1203
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0

DB:                       9          Gaps:            0

US-09-990-046-2 (1-1203) x AY358555 (1-3641)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 60

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 120

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 180

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 240

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 300

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 360

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 420

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 480

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 540

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 600

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 660

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 720

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 780

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 840

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGluGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 900

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 960

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1020

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
```

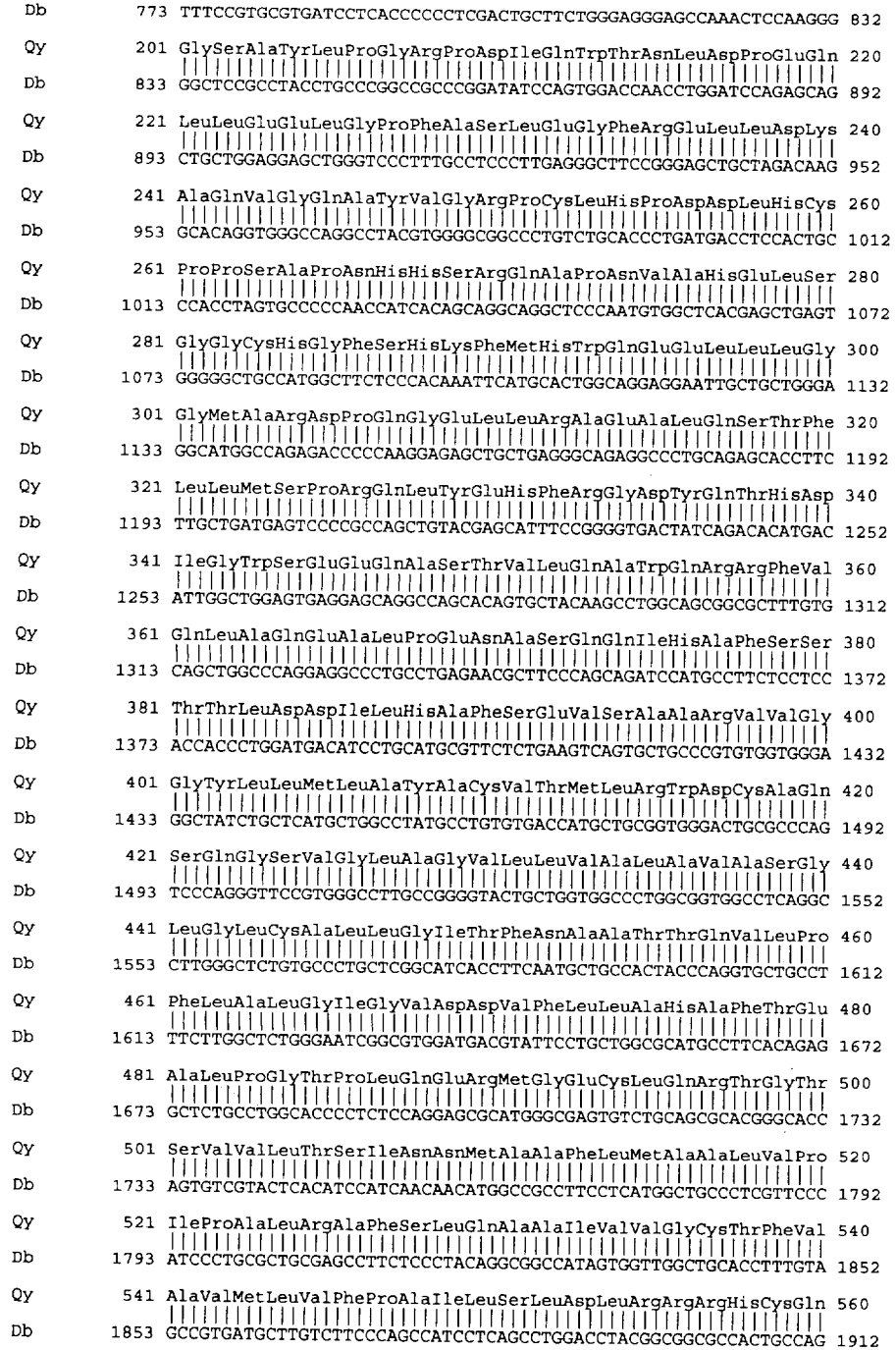

Db 1021 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1080
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1081 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1140
Qy 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1141 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1200
Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1201 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1260
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1261 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1320
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1321 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1380
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1381 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1440
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1441 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1500
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1501 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1560
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1561 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1620
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1621 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1680
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1681 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1740
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1741 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1800
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 1801 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1860
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 1861 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1920
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 1921 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1980
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 1981 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2040
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2041 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2100
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2101 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2160
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2161 ACCAAGGAGCACGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2220
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2221 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2280
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2281 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2340
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2341 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2400
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2401 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2460
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2461 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2520
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2521 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2580
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2581 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2640
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2641 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2700
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2701 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2760
Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2761 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2820
Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 2821 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2880
Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 2881 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2940
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 2941 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3000
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3001 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3060
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3061 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3120
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3121 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3180
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3181 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3240

```
Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db       3241 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3300

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db       3301 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3360

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db       3361 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3420

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db       3421 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3480

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db       3481 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3540

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db       3541 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3600

Qy       1201 AlaThrGly 1203
Db       3601 GCCACTGGG 3609
```

```
RESULT 3
AY359016
LOCUS       AY359016                3765 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA67654 Patched 2 (UNQ560) mRNA, complete cds.
ACCESSION   AY359016
VERSION     AY359016.1  GI:37183149
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3765)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 3765)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .3765
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA67654"
     gene            1. .3765
                     /locus_tag="UNQ560"
     CDS             5. .3616
                     /locus_tag="UNQ560"
                     /note="PRO57079"
                     /codon_start=1
                     /product="Patched 2"
                     /protein_id="AAQ89375.1"
                     /db_xref="GI:37183150"
                     /translation="MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLL
                     FSLGCGIQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKE
                     KLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKIC
                     YKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
                     EQLLEELGPFASLEGFRELLLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVA
                     HELSGGCHGFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG
                     DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSE
                     VSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
                     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSIN
                     NMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLC
                     CFSSPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLV
                     PPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQ
                     SHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
                     LVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQ
                     DWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELF
                     YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLL
                     RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
                     VCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGV
                     EFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF
                     FAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGAS
                     SSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGPATG"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:          3765
Score:                  6272.00        Matches:         1203
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     9              Gaps:            0

US-09-990-046-2 (1-1203) x AY359016 (1-3765)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db          5 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 64

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db         65 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 124

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db        125 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 184

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db        185 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 244

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db        245 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 304

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db        305 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 364

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db        365 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 424

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db        425 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 484

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db        485 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 544

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
```

```
Db        545 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 604
Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db        605 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 664
Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db        665 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 724
Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db        725 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 784
Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db        785 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 844
Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGluGly 300
Db        845 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 904
Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db        905 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 964
Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db        965 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1024
Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db       1025 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1084
Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db       1085 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1144
Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db       1145 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1204
Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db       1205 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1264
Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db       1265 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1324
Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db       1325 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1384
Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db       1385 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1444
Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db       1445 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1504
Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db       1505 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1564
Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db       1565 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1624
Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1625 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1684

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1685 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1744
Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1745 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1804
Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       1805 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1864
Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       1865 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1924
Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       1925 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1984
Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       1985 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2044
Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2045 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2104
Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2105 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2164
Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2165 ACCAAGGAGCACGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2224
Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2225 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2284
Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2285 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2344
Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2345 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2404
Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2405 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2464
Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2465 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2524
Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2525 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2584
Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2585 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2644
Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2645 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2704
Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2705 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2764
```

```
Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2765 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2824

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      2825 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2884

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      2885 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2944

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      2945 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3004

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3005 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3064

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3065 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3124

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3125 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3184

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3185 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3244

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3245 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3304

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3305 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3364

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3365 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3424

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3425 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3484

Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3485 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3544

Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3545 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3604

Qy      1201 AlaThrGly 1203
Db      3605 GCCACTGGG 3613

RESULT 4
BD194644
LOCUS       BD194644                4030 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Vertebrate PATCHED-2 protein.
ACCESSION   BD194644
VERSION     BD194644.1  GI:33004389
KEYWORDS    JP 2002511263-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4030)
  AUTHORS   Soberge,F.J.D. and Carpenter,D.A.
  TITLE     Vertebrate PATCHED-2 protein
  JOURNAL   Patent: JP 2002511263-A 1 16-APR-2002;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002511263-A/1
            PD   16-APR-2002
            PF   02-APR-1999 JP 2000543606
            PR   15-APR-1998 US    09/060939
            PI   FREDERICK J DE SOBERGE,DAVID A CARPENTER
            PC   C12N15/09,C07K14/705,C07K16/00,C07K19/00,C12N1/19,C12N1/21, PC
              C12N5/10,
            PC   C12P21/02,C12Q1/02,G01N33/15,G01N33/50,G01N33/68//(C12P21/02,
            PC   C12R1:645),
            PC   (C12P21/02,C12R1:19),(C12P21/02,C12R1:91),C12N15/00,C12N5/00
            CC   Vertebrate PATCHED-2 protein
            FH   Key             Location/Qualifiers
            FT   source          1. .4030
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .4030
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4030
Score:                    6272.00        Matches:         1203
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-990-046-2 (1-1203) x BD194644 (1-4030)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db        233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db        293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db        353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db        413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db        473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db        533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db        593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db        653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db        713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
```


Db 773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832
Qy 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
Qy 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGluGly 300
Db 1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372
Qy 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432
Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

```
Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3533 CTCCATGGACTCGTGCTGCTGCCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy      1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy      1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy      1201 AlaThrGly 1203
Db      3833 GCCACTGGG 3841

RESULT 5
AR194379
LOCUS       AR194379                4030 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6348575.
ACCESSION   AR194379
VERSION     AR194379.1  GI:20240971
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4030)
  AUTHORS   de Sauvage,F. and Carpenter,D.A.
  TITLE     Patched-2
  JOURNAL   Patent: US 6348575-A 1 19-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .4030
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4030
Score:                    6272.00        Matches:         1203
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-990-046-2 (1-1203) x AR194379 (1-4030)

Qy         1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db       233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy        21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db       293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy        41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db       353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy        61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db       413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy        81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db       473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy       101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db       533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy       121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db       593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy       141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db       653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy       161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db       713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy       181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db       773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy       201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db       833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892

Qy       221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db       893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952

Qy       241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db       953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012

Qy       261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db      1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072
```

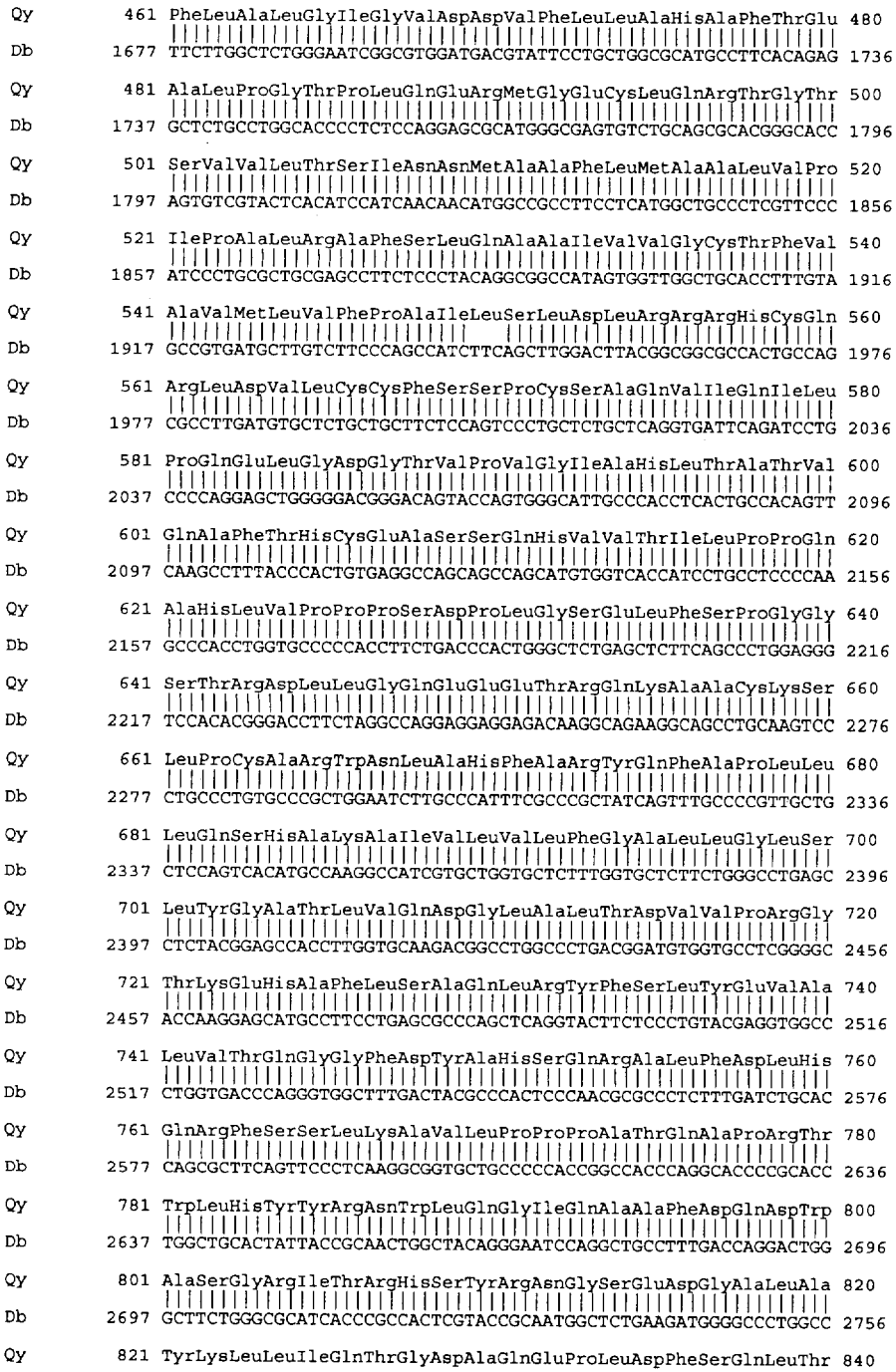
```
Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGlyGly 300
Db       1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db       1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db       1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db       1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db       1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db       1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db       1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db       1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db       1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db       1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db       1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db       1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db       1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852

Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db       1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db       1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db       1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db       2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db       2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db       2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db       2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272

Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db       2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332

Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db       2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392

Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db       2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452

Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db       2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512

Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db       2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db       2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db       2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db       2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db       2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db       2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db       2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932

Qy        901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db       2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db       2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db       3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db       3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db       3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
```

```
Db       3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 ACCGTGGCCATCCACCCACCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3833 GCCACTGGG 3841

RESULT 6
AR489133
LOCUS       AR489133                4030 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 1 from patent US 6709838.
ACCESSION   AR489133
VERSION     AR489133.1  GI:47256039
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4030)
  AUTHORS   de Sauvage,F. and Carpenter,D.A.
  TITLE     Nucleic acid encoding patched-2
  JOURNAL   Patent: US 6709838-A 1 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .4030
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4030
Score:                    6272.00        Matches:         1203
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-990-046-2 (1-1203) x AR489133 (1-4030)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       233 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 292

Qy        21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       293 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

Qy        41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       353 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 412

Qy        61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       413 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 472

Qy        81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       473 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 532

Qy       101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       533 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592

Qy       121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       593 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 652

Qy       141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 712

Qy       161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       713 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGTGGATGATTGAGAAGCTG 772

Qy       181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       773 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 832

Qy       201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       833 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892

Qy       221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       893 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952

Qy       241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       953 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1012

Qy       261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1013 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1072

Qy       281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1073 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1132

Qy       301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1133 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192

Qy       321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1193 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252

Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1253 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1312

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1313 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1372

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1373 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1432

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1433 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1492

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1493 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1552

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1553 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1613 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1672

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1673 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1732

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1733 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1792

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1793 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1852

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1853 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1912

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1913 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1972

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1973 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2032

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2092

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      2093 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      2153 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2212

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      2213 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2272

Qy       681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db      2273 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2332

Qy       701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db      2333 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2392

Qy       721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db      2393 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452

Qy       741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db      2453 CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCCCAACGCGCCCTCTTTGATCTGCAC 2512

Qy       761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db      2513 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2572

Qy       781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db      2573 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2632

Qy       801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db      2633 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy       821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db      2693 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2752

Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2753 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812

Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2813 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872

Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db      2873 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2932

Qy       901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2933 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2992

Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3052

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      3053 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3112

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      3113 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3172

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      3173 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3232

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3233 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3292

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3293 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3353 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3412

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3413 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3472

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3473 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3532
```

```
Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3592

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3652

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3712

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3772

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832

Qy       1201 AlaThrGly 1203
             |||||||||
Db       3833 GCCACTGGG 3841

RESULT 7
AR175919
LOCUS       AR175919                4391 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6309879.
ACCESSION   AR175919
VERSION     AR175919.1  GI:17917218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4391)
  AUTHORS   Bumcrot,D.H.
  TITLE     Human patched genes and proteins, and uses related thereto
  JOURNAL   Patent: US 6309879-A 1 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .4391
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4391
Score:                    6248.00        Matches:         1200
Percent Similarity:       99.75%         Conservative:    0
Best Local Similarity:    99.75%         Mismatches:      3
Query Match:              99.62%         Indels:          0
DB:                       6              Gaps:            0

US-09-990-046-2 (1-1203) x AR175919 (1-4391)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676
```


Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056
Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116
Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176
Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536
Qy 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596
Qy 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db 3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656
Qy 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db 3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716
Qy 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776
Qy 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836
Qy 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200

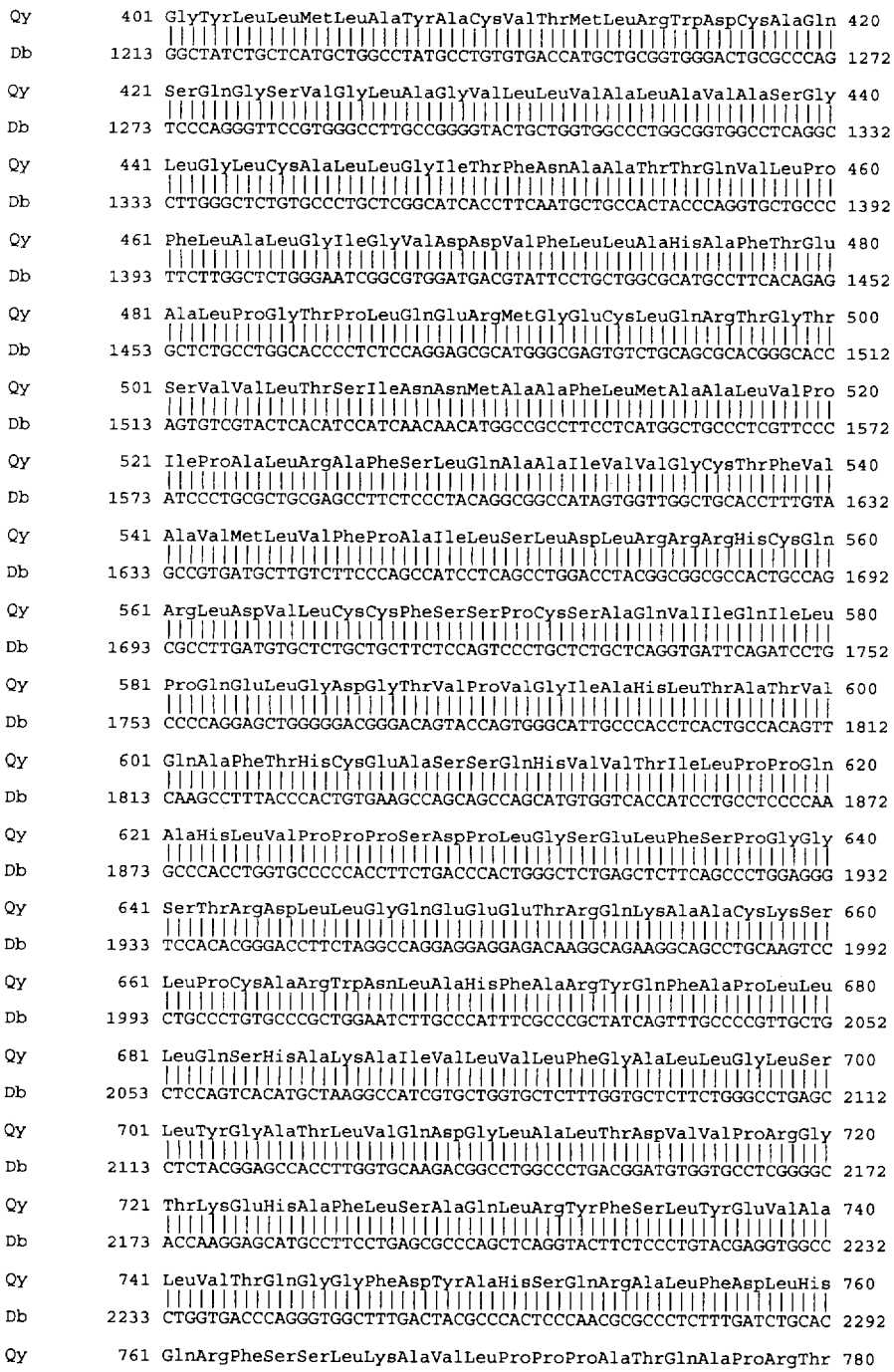
```
Db       3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3897 GCCACTGGG 3905

RESULT 8
AR374936
LOCUS       AR374936                4391 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6605700.
ACCESSION   AR374936
VERSION     AR374936.1  GI:40078100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4391)
  AUTHORS   Bumcrot,D.A.
  TITLE     Human patched genes and proteins, and uses related thereto
  JOURNAL   Patent: US 6605700-A 1 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .4391
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0             Length:          4391
Score:                    6248.00       Matches:         1200
Percent Similarity:       99.75%        Conservative:    0
Best Local Similarity:    99.75%        Mismatches:      3
Query Match:              99.62%        Indels:          0
DB:                       6             Gaps:            0

US-09-990-046-2 (1-1203) x AR374936 (1-4391)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 356

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 476

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 536

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 596

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 656

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 716

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 776

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        777 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 836

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 896

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 1016

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 1076

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 1136

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 1196

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1316

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1376

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1377 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1436

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1437 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1496

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1556

Qy        421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1557 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1616

Qy        441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1617 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1676

Qy        461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1677 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1736

Qy        481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1737 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1796

Qy        501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1797 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1856

Qy        521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1857 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1916

Qy        541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
```

```
Db       1917 GCCGTGATGCTTGTCTTCCCAGCCATCTTCAGCTTGGACTTACGGCGGCGCCACTGCCAG 1976

Qy        561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1977 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 2036

Qy        581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2037 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 2096

Qy        601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2097 CAAGCCTTTACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 2156

Qy        621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2157 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2216

Qy        641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2217 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 2276

Qy        661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2277 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2336

Qy        681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2337 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2396

Qy        701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2397 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2456

Qy        721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2457 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2516

Qy        741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2517 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2576

Qy        761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2577 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2636

Qy        781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2637 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2696

Qy        801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2697 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAAGATGGGGCCCTGGCC 2756

Qy        821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2757 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2816

Qy        841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2817 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2876

Qy        861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2877 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2936

Qy        881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2937 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2996

Qy        901 ProAlaGlnProLeuGluPheAlaGlnProProPheLeuLeuArgGlyLeuGlnLysThr 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2997 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 3056

Qy        921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3057 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 3116

Qy        941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3117 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 3176

Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3177 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 3236

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3237 CTGCTGCTCCTCAACCCCTGGATGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3296

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3297 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3356

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3357 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3416

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3417 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3476

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3477 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3536

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3537 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3596

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3597 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3656

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3657 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3716

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3717 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3776

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3777 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3836

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3837 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3896

Qy       1201 AlaThrGly 1203
              |||||||||
Db       3897 GCCACTGGG 3905

RESULT 9
AF087651
LOCUS       AF087651               3612 bp    mRNA    linear   PRI 20-APR-1999
DEFINITION  Homo sapiens patched 2 (PTCH2) mRNA, complete cds.
ACCESSION   AF087651
VERSION     AF087651.1  GI:4588014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3612)
```

```
  AUTHORS   Smyth,I., Narang,M.A., Evans,T., Heimann,C., Nakamura,Y.,
            Chenevix-Trench,G., Pietsch,T., Wicking,C. and Wainwright,B.J.
  TITLE     Isolation and characterization of human patched 2 (PTCH2), a
            putative tumour suppressor gene inbasal cell carcinoma and
            medulloblastoma on chromosome 1p32
  JOURNAL   Hum. Mol. Genet. 8 (2), 291-297 (1999)
  MEDLINE   99135908
   PUBMED   9931336
REFERENCE   2  (bases 1 to 3612)
  AUTHORS   Smyth,I., Narang,M.A., Evans,T., Heimann,C., Nakamura,Y.,
            Chenevix-Trench,G., Pietsch,T., Wicking,C. and Wainwright,B.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-1998) Center for Molecular and Cellular Biology,
            University of Queensland, Ritchie Laboratories, Research Rd.,
            Brisbane, QLD 4072, Australia
FEATURES             Location/Qualifiers
     source          1. .3612
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p32"
     gene            1. .3612
                     /gene="PTCH2"
     CDS             1. .3612
                     /gene="PTCH2"
                     /codon_start=1
                     /product="patched 2"
                     /protein_id="AAD25953.1"
                     /db_xref="GI:4588015"
                     /translation="MNRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLL
                     FSLGCGIQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKE
                     KLGEEAAYTSQMLIQTALQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKIC
                     YKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
                     EQLLEELGPFASLEGFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVA
                     HELSGGCHGFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG
                     DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSE
                     VSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
                     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSIN
                     NMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLC
                     CFSSPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLV
                     PPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQ
                     SHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
                     LVTQGGFDYAHSRRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQ
                     DWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFGQLTTRKLVEREGLIPPELF
                     YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPFLL
                     RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
                     VCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGV
                     EFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF
                     FAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGAS
                     SSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGPATG"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          3612
Score:                    6229.00        Matches:         1196
Percent Similarity:       99.67%         Conservative:    3
Best Local Similarity:    99.42%         Mismatches:      4
Query Match:              99.31%         Indels:          0
DB:                       9              Gaps:            0

US-09-990-046-2 (1-1203) x AF087651 (1-3612)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 60

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 120

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 180

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 240

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 300

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACTC 360

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 420

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATTTGC 480

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        481 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 540

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 600

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 660

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 720

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 780

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 840

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 900

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 960

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1020

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1080

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1140

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1200

Qy        401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1260
```

```
Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1261 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1320

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1321 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1380

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1381 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1440

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1441 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1500

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1501 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1560

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1561 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1620

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1621 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1680

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1681 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1740

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1741 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1800

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1801 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1860

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1861 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1920

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1921 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1980

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1981 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2040

Qy       681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db      2041 CTCCAGTCACATGCCAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2100

Qy       701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db      2101 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2160

Qy       721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db      2161 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2220

Qy       741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db      2221 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCGACGCGCCCTCTTTGATCTGCAC 2280

Qy       761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db      2281 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2340

Qy       781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db      2341 TGGCTGCACTATTACCGCAGCTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2400

Qy       801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db      2401 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2460

Qy       821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db      2461 TACAAGCTGCTCATCCAGACTGGAGATGCCCAGGAGCCTCTGGATTTCGGCCAGCTGACC 2520

Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2521 ACAAGGAAGCTGGTGGAGAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2580

Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2581 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2640

Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db      2641 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCG 2700

Qy       901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2701 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2760

Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2761 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2820

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      2821 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2880

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      2881 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2940

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      2941 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3000

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3001 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3060

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3061 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3120

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3121 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3180

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3181 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3240

Qy      1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3241 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3300

Qy      1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db      3301 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3360

Qy      1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
Db      3361 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3420

Qy      1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
```

```
Db       3421 CTTAGGTGGGGGGCATCCTCCTCCCTGCCCCAGAGCTTTGCCAGAGTGACTACCTCCATG 3480

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180

Db       3481 ACCGTGGCCATCCACCCACCCCCCCTGCCTGGTGCCTACATCCATCCAGCCCCTGATGAG 3540

Qy       1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200

Db       3541 CCCCCTTGGTCCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAGGTCCA 3600

Qy       1201 AlaThrGly 1203

Db       3601 GCCACTGGG 3609

RESULT 10
BD227641
LOCUS       BD227641               3453 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel constitutional elements in hedgehog transmission pathway.
ACCESSION   BD227641
VERSION     BD227641.1  GI:33037411
KEYWORDS    JP 2002526050-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3453)
  AUTHORS   Zaphiropoulos,P.G., Unden,A.B., Toftgard,R., Rahnama,F. and
            Hollingsworth,R.E.
  TITLE     Novel constitutional elements in hedgehog transmission pathway
  JOURNAL   Patent: JP 2002526050-A 1 20-AUG-2002;
            KAROLINSKA INNOVATIONS AB,PHARMACIA AND UPJOHN CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526050-A/1
            PD   20-AUG-2002
            PF   06-OCT-1999 JP 2000573395
            PR   06-OCT-1998 SE    9803393-9
            PI   PETER G ZAPHIROPOULOS,ANNE BIRGITTE UNDEN,RUNE TOFTGARD, PI
            FAHIMEH RAHNAMA,
            PI   ROBERT E HOLLINGSWORTH
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P25/16,A61P35/00,
            PC   C07K14/705,
            PC   C07K16/28,C12N5/10,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
             G01N33/53,
            PC   G01N33/58,G01N37/00,C12N15/00,A61K37/02,C12N5/00 CC   Novel
            constitutional elements in hedgehog transmission pathway FH   Key
                     Location/Qualifiers
            FT   source          1. .3453
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .3453
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         3453
Score:                  5911.00        Matches:        1139
Percent Similarity:     99.74%         Conservative:   0
Best Local Similarity:  99.74%         Mismatches:     3
Query Match:            94.24%         Indels:         0
DB:                     6              Gaps:           0

US-09-990-046-2 (1-1203) x BD227641 (1-3453)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20

Db         13 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 72

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40

Db         73 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 132

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60

Db        133 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 192

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80

Db        193 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 252

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100

Db        253 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 312

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120

Db        313 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 372

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140

Db        373 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 432

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160

Db        433 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 492

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180

Db        493 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 552

Qy        181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200

Db        553 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 612

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220

Db        613 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 672

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240

Db        673 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 732

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260

Db        733 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 792

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280

Db        793 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 852

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300

Db        853 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 912

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320

Db        913 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 972

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340

Db        973 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1032

Qy        341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360

Db       1033 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1092

Qy        361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380

Db       1093 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1152

Qy        381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400

Db       1153 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1212
```


Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1213 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1272
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1273 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1332
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1333 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1392
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1393 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1452
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1453 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1512
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1513 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1572
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1573 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1632
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1633 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1692
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1693 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1752
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1753 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1812
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 1813 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1872
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 1873 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1932
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 1933 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1992
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 1993 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2052
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2053 CTCCAGTCACATGCTAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2112
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2113 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2172
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2173 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2232
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2233 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2292
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2293 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2352
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2353 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2412
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2413 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2472
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2473 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCTTCTGGATTTCAGCCAGCTGACC 2532
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2533 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2592
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2593 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2652
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2653 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACTTTCGCATCCCG 2712
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2713 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2772
Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2773 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2832
Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 2833 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2892
Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 2893 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2952
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 2953 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3012
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3013 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3072
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3073 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3132
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3133 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3192
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3193 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3252
Qy 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3253 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3312
Qy 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
Db 3313 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3372
Qy 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140

```
Db       3373 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3432

Qy       1141 LeuArg 1142
              ||||||
Db       3433 CTTAGG 3438

RESULT 11
AF119569
LOCUS       AF119569                3453 bp    mRNA    linear   PRI 31-MAR-1999
DEFINITION  Homo sapiens patched 2 (PTCH2) mRNA, complete cds.
ACCESSION   AF119569
VERSION     AF119569.1  GI:4325110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3453)
  AUTHORS   Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
            Toftgard,R.
  TITLE     PTCH2, a novel human patched gene, undergoing alternative splicing
            and up-regulated in basal cell carcinomas
  JOURNAL   Cancer Res. 59 (4), 787-792 (1999)
  MEDLINE   99151521
   PUBMED   10029063
REFERENCE   2  (bases 1 to 3453)
  AUTHORS   Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
            Toftgard,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-1999) Bioscience, Karolinska, Huddinge 141 57,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .3453
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p33-p34"
     gene            1. .3453
                     /gene="PTCH2"
     CDS             13. .3453
                     /gene="PTCH2"
                     /codon_start=1
                     /product="patched 2"
                     /protein_id="AAD17260.1"
                     /db_xref="GI:4325111"
                     /translation="MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLL
                     FSLGCGIQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKE
                     KLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKIC
                     YKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
                     EQLLEELGPFASLEGFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVA
                     HELSGGCHGFSHKFMHWQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG
                     DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSE
                     VSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
                     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSIN
                     NMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLC
                     CFSSPCSAQVIQILPQELGDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLV
                     PPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQ
                     SHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
                     LVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQ
                     DWASGRITRHSYRNGSEDGALAYKLLIQTGDAQELLDFSQLTTRKLVDREGLIPPELF
                     YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENFRIPPAQPLEFAQFPFLL
                     RGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
                     VCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGV
                     EFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYF
                     FAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRPEEI
                     "
ORIGIN

Alignment Scores:
Pred. No.:              0           Length:        3453
Score:                  5911.00     Matches:       1139
Percent Similarity:     99.74%      Conservative:  0

Best Local Similarity:  99.74%      Mismatches:    3
Query Match:            94.24%      Indels:        0
DB:                     9           Gaps:          0

US-09-990-046-2 (1-1203) x AF119569 (1-3453)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 ATGACTCGATCGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC 72

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GCAGCACCCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 132

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CAGGGCCTGCTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTT 192

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTGGGACTGTTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACA 252

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 AACTTGGAACAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACC 312

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 372

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTC 432

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGC 492

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        493 TACAAGTCAGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 552

Qy        181 ProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TTTCCGTGCGTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGG 612

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GGCTCCGCCTACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 672

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGCTGGAGGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAG 732

Qy        241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GCACAGGTGGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGC 792

Qy        261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 CCACCTAGTGCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGT 852

Qy        281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 GGGGGCTGCCATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 912

Qy        301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 GGCATGGCCAGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 972

Qy        321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 TTGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1032
```

```
Qy       341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db      1033 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTG 1092

Qy       361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db      1093 CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCC 1152

Qy       381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db      1153 ACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGA 1212

Qy       401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db      1213 GGCTATCTGCTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAG 1272

Qy       421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db      1273 TCCCAGGGTTCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGC 1332

Qy       441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db      1333 CTTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCC 1392

Qy       461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db      1393 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAG 1452

Qy       481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db      1453 GCTCTGCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1512

Qy       501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db      1513 AGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCC 1572

Qy       521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db      1573 ATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTA 1632

Qy       541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db      1633 GCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG 1692

Qy       561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db      1693 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1752

Qy       581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db      1753 CCCCAGGAGCTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTT 1812

Qy       601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db      1813 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAA 1872

Qy       621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db      1873 GCCCACCTGGTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1932

Qy       641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db      1933 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCC 1992

Qy       661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db      1993 CTGCCCTGTGCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTG 2052

Qy       681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db      2053 CTCCAGTCACATGCTAAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGC 2112

Qy       701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db      2113 CTCTACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGC 2172

Qy       721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db      2173 ACCAAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2232

Qy       741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db      2233 CTGGTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2292

Qy       761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db      2293 CAGCGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACC 2352

Qy       781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db      2353 TGGCTGCACTATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGG 2412

Qy       801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db      2413 GCTTCTGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2472

Qy       821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db      2473 TACAAGCTGCTCATCCAGACTGGAGACGCCCAGGAGCTTCTGGATTTCAGCCAGCTGACC 2532

Qy       841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2533 ACAAGGAAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2592

Qy       861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2593 ACCGTGTGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2652

Qy       881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db      2653 CCACCTCCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACTTTCGCATCCCG 2712

Qy       901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2713 CCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACT 2772

Qy       921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2773 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCT 2832

Qy       941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      2833 GGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTG 2892

Qy       961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      2893 CGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCT 2952

Qy       981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      2953 CTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACA 3012

Qy      1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3013 GTGGAACTCTTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTG 3072

Qy      1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3073 ATCCTTGTGGCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3132

Qy      1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db      3133 CTGACCACCCAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCC 3192

Qy      1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3193 CCCGTGACCGATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCAC 3252

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 TTTGACTTCATTGTAAGGTACTTCTTTGCGGCGCTGACAGTGCTCACGCTCCTGGGCCTC 3312

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 CTCCATGGACTCGTGCTGCTGCCTGTGCTGCTGTCCATCCTGGGCCCGCCGCCAGAGGTG 3372

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3373 ATACAGATGTACAAGGAAAGCCCAGAGATCCTGAGTCCACCAGCTCCACAGGGAGGCGGG 3432

Qy       1141 LeuArg 1142
                ||||||
Db       3433 CTTAGG 3438
```

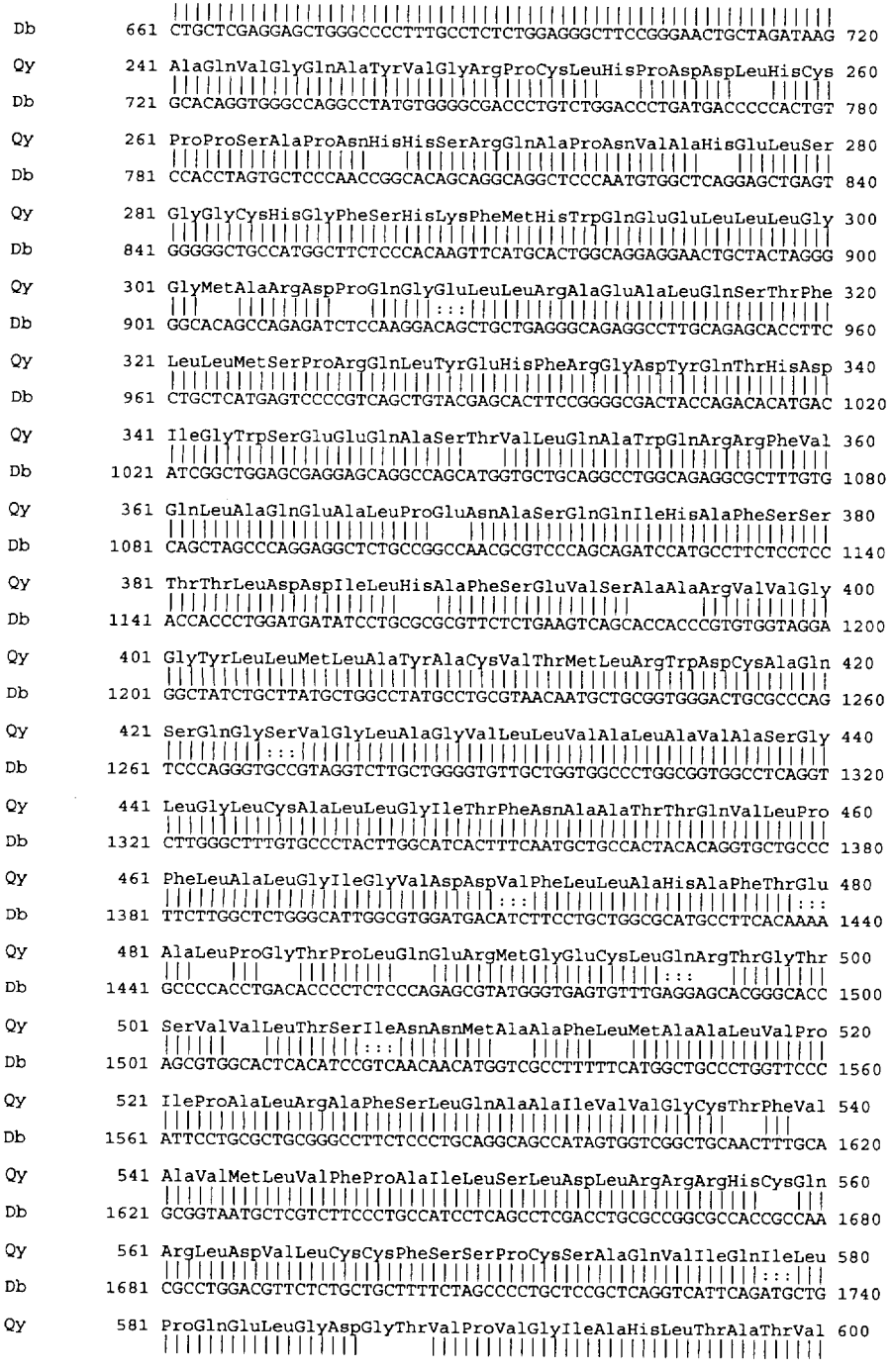
RESULT 12
AB010833
LOCUS AB010833 3549 bp mRNA linear ROD 13-FEB-1999
DEFINITION Mus musculus ptch2 mRNA, complete cds.
ACCESSION AB010833 AB000847
VERSION AB010833.1 GI:2842557
KEYWORDS ptch2.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Takabatake,T., Ogawa,M., Takahashi,T.C., Mizuno,M., Okamoto,M. and Takeshima,K.
TITLE Hedgehog and patched gene expression in adult ocular tissues
JOURNAL FEBS Lett. 410 (2-3), 485-489 (1997)
MEDLINE 97379366
PUBMED 9237688
REFERENCE 2 (sites)
AUTHORS Motoyama,J., Takabatake,T., Takeshima,K. and Hui,C.
TITLE Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog
JOURNAL Nat. Genet. 18 (2), 104-106 (1998)
MEDLINE 98122566
PUBMED 9462734
REFERENCE 3 (bases 1 to 3549)
AUTHORS Takabatake,T.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1998) Takashi Takabatake, Nagoya University, Radioisotope Research Center; Furo-cho, Chikusa, Nagoya, Aichi 464-8602, Japan (E-mail:j45998a@nucc.cc.nagoya-u.ac.jp, Tel:052-789-2573, Fax:052-789-2567)
COMMENT On Feb 6, 1998 this sequence version replaced gi:2598660.
AB000847: Submitted (04-Feb-1997).
FEATURES Location/Qualifiers
source 1. .3549
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/cCrSlc"
/db_xref="taxon:10090"
/dev_stage="14dpc"
gene 1. .3549
/gene="ptch2"
CDS 1. .3549
/gene="ptch2"
/note="putative twelve transmembrane domain protein"
/codon_start=1
/protein_id="BAA24691.1"
/db_xref="GI:2842558"
/translation="MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLL
FSLGCRIQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKE
KLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKIC
YKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDP
QQLLEELGPFASLEGFRELLDKAQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVA
QELSGGCHGFSHKFMHWQEELLLGGTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRG
DYQTHDIGWSEEQASMVLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSE
VSTTRVVGGYLLMLAYACVTMLRWDCAQSQGAVGLAGVLLVALAVASGLGLCALLGIT
FNAATTQVLPFLALGIGVDDIFLLAHAFTKAPPDTPLPERMGECLRSTGTSVALTSVN
NMVAFFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAILSLDLRRRHRQRLDVLC
CFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHLL
SPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRPLLCAHWTLAHFARYQFAPLLLQ
TRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVA
LVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQ
DWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLVDKEGLIPPELF
YMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPAAQPLEFAQFPFLL
HGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILL
VCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASIGIGV
EFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYF
FVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRP
PTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEPT"
ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	3549
Score:	5599.00	Matches:	1074
Percent Similarity:	94.58%	Conservative:	43
Best Local Similarity:	90.94%	Mismatches:	64
Query Match:	89.27%	Indels:	0
DB:	10	Gaps:	0

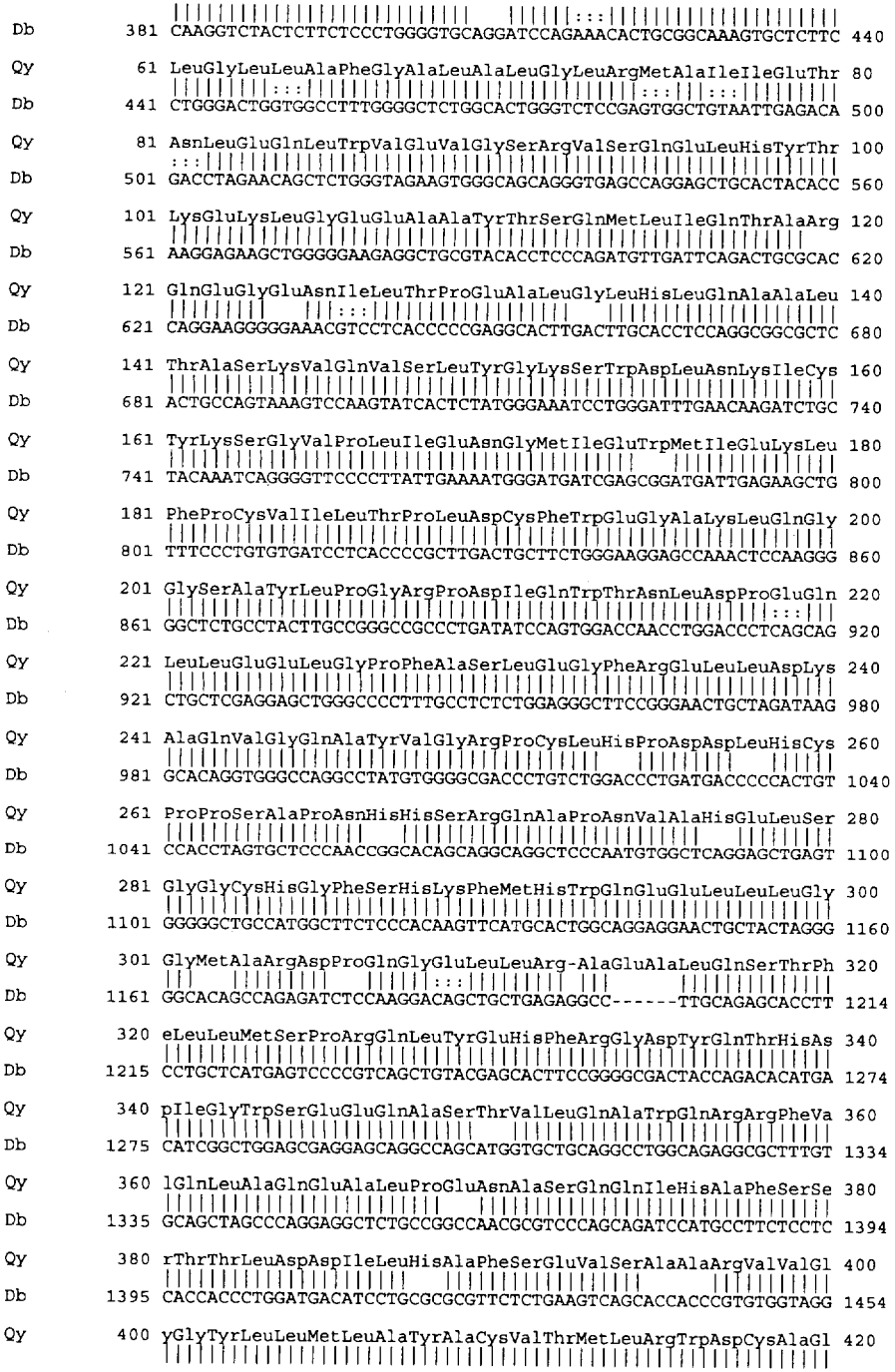
US-09-990-046-2 (1-1203) x AB010833 (1-3549)

```
Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              |||  |||         |||  ||||||||||||||||||||||||||||||||:::
Db          1 ATGGTTCGGCCACTGTCCCTTGGAGAGCTACCTCCCAGCTACACACCTCCAGCTCGGTCC 60

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              :::||||||  ||||||||||||||||||:::||||||||||||||||||||||||||||
Db         61 TCCGCACCTCATATCCTAGCTGGGAGCCTGCAGGCTCCTCTCTGGCTTCGAGCTTACTTC 120

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
              ||||||||||||||||||||||||||||||  ||||||:::||||||||||||||||||||
Db        121 CAAGGTCTACTCTTCTCCCTGGGGTGCAGGATCCAGAAACACTGCGGCAAAGTGCTCTTC 180

Qy         61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
              |||||||||:::|||||||||||||||||||||||||||||:::|||:::||||||||||
Db        181 CTGGGACTGGTGGCCTTTGGGGCTCTGGCACTGGGTCTCCGAGTGGCTGTAATTGAGACA 240

Qy         81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCTAGAACAGCTCTGGGTAGAAGTGGGCAGCAGGGTGAGCCAGGAGCTGCACTACACC 300

Qy        101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGAGAAGCTGGGGGAAGAGGCTGCGTACACCTCCCAGATGTTGATTCAGACTGCGCAC 360

Qy        121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
              ||||||||  |||:::||||||||||||||||||  ||||||||||||||||||||||||
Db        361 CAGGAAGGGGGAAACGTCCTCACCCCCGAGGCACTTGACTTGCACCTCCAGGCGGCGCTC 420

Qy        141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAATCCTGGGATTTGAACAAGATCTGC 480

Qy        161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        481 TACAAATCAGGGGTTCCCCTTATTGAAAATGGGATGATCGAACGGATGATTGAGAAGCTG 540

Qy        181 ProProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTCCCTGTGTGATCCTCACCCCGCTTGACTGCTTCTGGGAAGGAGCCAAACTCCAAGGG 600

Qy        201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        601 GGCTCTGCCTACTTGCCGGGCCGCCCTGATATCCAGTGGACCAACCTGGACCCTCAGCAG 660

Qy        221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
```


Db 661 CTGCTCGAGGAGCTGGGCCCCTTTGCCTCTCTGGAGGGCTTCCGGGAACTGCTAGATAAG 720
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 721 GCACAGGTGGGCCAGGCCTATGTGGGGCGACCCTGTCTGGACCCTGATGACCCCCACTGT 780
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 781 CCACCTAGTGCTCCCAACCGGCACAGCAGGCAGGCTCCCAATGTGGCTCAGGAGCTGAGT 840
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 841 GGGGGCTGCCATGGCTTCTCCCACAAGTTCATGCACTGGCAGGAGGAACTGCTACTAGGG 900
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 901 GGCACAGCCAGAGATCTCCAAGGACAGCTGCTGAGGGCAGAGGCCTTGCAGAGCACCTTC 960
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 961 CTGCTCATGAGTCCCCGTCAGCTGTACGAGCACTTCCGGGGCGACTACCAGACACATGAC 1020
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 1021 ATCGGCTGGAGCGAGGAGCAGGCCAGCATGGTGCTGCAGGCCTGGCAGAGGCGCTTTGTG 1080
Qy 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1081 CAGCTAGCCCAGGAGGCTCTGCCGGCCAACGCGTCCCAGCAGATCCATGCCTTCTCCTCC 1140
Qy 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1141 ACCACCCTGGATGATATCCTGCGCGCGTTCTCTGAAGTCAGCACCACCCGTGTGGTAGGA 1200
Qy 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1201 GGCTATCTGCTTATGCTGGCCTATGCCTGCGTAACAATGCTGCGGTGGGACTGCGCCCAG 1260
Qy 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1261 TCCCAGGGTGCCGTAGGTCTTGCTGGGGTGTTGCTGGTGGCCCTGGCGGTGGCCTCAGGT 1320
Qy 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1321 CTTGGGCTTTGTGCCCTACTTGGCATCACTTTCAATGCTGCCACTACACAGGTGCTGCCC 1380
Qy 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1381 TTCTTGGCTCTGGGCATTGGCGTGGATGACATCTTCCTGCTGGCGCATGCCTTCACAAAA 1440
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1441 GCCCCACCTGACACCCCTCTCCCAGAGCGTATGGGTGAGTGTTTGAGGAGCACGGGCACC 1500
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1501 AGCGTGGCACTCACATCCGTCAACAACATGGTCGCCTTTTTCATGGCTGCCCTGGTTCCC 1560
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1561 ATTCCTGCGCTGCGGGCCTTCTCCCTGCAGGCAGCCATAGTGGTCGGCTGCAACTTTGCA 1620
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db 1621 GCGGTAATGCTCGTCTTCCCTGCCATCCTCAGCCTCGACCTGCGCCGGCGCCACCGCCAA 1680
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1681 CGCCTGGACGTTCTCTGCTGCTTTTCTAGCCCCTGCTCCGCTCAGGTCATTCAGATGCTG 1740
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1741 CCCCAGGAGCTAGGGGACAGAGCAGTACCAGTGGGCATTGCCCACCTGACTGCCACCGTG 1800
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 1801 CAAGCCTTCACCCACTGCGAAGCCAGCAGCCAGCATGTAGTCACCATTTTGCCTCCTCAA 1860
Qy 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 1861 GCCCACCTGCTGTCTCCAGCTTCTGACCCACTGGGCTCCGAACTCTATAGCCCTGGAGGG 1920
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 1921 TCTACACGGGACCTTCTCAGTCAGGAGGAGGGGACAGGGCCACAGGCGGCCTGCAGGCCC 1980
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 1981 CTGCTCTGTGCCCACTGGACTCTCGCCCATTTTGCCCGCTATCAGTTTGCACCTTTACTG 2040
Qy 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2041 CTCCAGACACGAGCCAAGGCCCTGGTGTTGCTGTTCTTTGGGGCTCTTTTGGGCCTGAGC 2100
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2101 CTCTATGGAGCCACCTTGGTACAAGATGGGCTGGCCCTGACAGATGTGGTCCCTAGGGGC 2160
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2161 ACCAAGGAACATGCTTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCT 2220
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2221 CTAGTGACACAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCAC 2280
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThr 780
Db 2281 CAGCGCTTCAGCTCCCTCAAGGCTGTGCTGCCCCCACCTGCCACCCAGGCACCCCGCACC 2340
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2341 TGGCTTCACTACTACCGCAGCTGGCTACAGGGTATCCAGGCTGCATTTGACCAAGACTGG 2400
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2401 GCTTCTGGGCGCATCACCTGCCACTCTTACCGCAACGGCTCAGAAGATGGCGCCCTGGCC 2460
Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2461 TACAAGCTGCTCATCCAAACCGGGAATGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACC 2520
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2521 ACAAGGAAACTGGTGGACAAGGAGGGACTCATTCCCCCAGAGCTCTTCTACATGGGGCTA 2580
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2581 ACCGTGTGGGTGAGCAGCGACCCCCTGGGCCTCGCAGCCTCTCAGGCCAACTTCTACCCC 2640
Qy 881 ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2641 CCACCTCCAGAGTGGCTTCACGACAAATATGATACCACCGGGGAGAACCTTCGCATCCCG 2700
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2701 GCAGCCCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCATGGACTCCAGAAGACT 2760
Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2761 GCAGACTTTGTAGAAGCCATCGAAGGGGCCAGGGCGGCATGCACAGAGGCAGGCCAGGCA 2820
Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 2821 GGGGTGCATGCCTACCCCAGTGGCTCCCCCTTCCTCTTCTGGGAGCAGTATCTGGGTCTT 2880

```
Qy        961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CGGCGCTGCTTCCTGCTGGCAGTCTGCATCTTGCTGGTGTGCACCTTCCTCGTCTGTGCC 2940

Qy        981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CTGCTTCTACTCAGCCCGTGGACAGCTGGCCTCATAGTGCTGGTCCTGGCAATGATGACT 3000

Qy       1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GTGGAGCTCTTTGGTATCATGGGATTCCTGGGCATCAAACTGAGTGCCATCCCCGTGGTA 3060

Qy       1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       3061 ATCCTCGTGGCCTCTATAGGCATTGGTGTTGAATTCACAGTTCACGTGGCTCTGGGCTTC 3120

Qy       1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
              ||||||:::  ||||||||||||||||||||||  ||||||||  ||||||||||||||||
Db       3121 CTGACCAGCCATGGTAGCCGGAACCTGCGGGCTGCTAGCGCTCTGGAACAGACCTTTGCC 3180

Qy       1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||:::
Db       3181 CCTGTGACTGATGGAGCTGTCTCCACCTTGCTGGGTCTGCTCATGCTTGCTGGTTCTAAC 3240

Qy       1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
              ||||||||||||:::||||||||||||      ||||||||||||||||||||||||||||||
Db       3241 TTTGACTTCATCATAAGGTATTTCTTTGTGGTGCTGACGGTGCTGACACTCTTGGGCCTG 3300

Qy       1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal 1120
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||:::|||
Db       3301 CTCCATGGACTCCTGCTGCTGCCTGTGCTGCTCTCTATCCTAGGCCCCCCGCCACAGGTG 3360

Qy       1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
              :::|||:::|||||||||||||||:::   |||:::      |||||||||   ||||||
Db       3361 GTGCAGGTATACAAGGAGAGTCCACAGACCCTAAACTCCGCTGCTCCACAGAGAGGTGGG 3420

Qy       1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
              |||||||||           :::||||||||||||||||||||||||||||||||||||||
Db       3421 CTCAGGTGGGACAGGCCCCCCACCCTGCCCCAGAGTTTTGCCAGAGTGACTACCTCCATG 3480

Qy       1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
              |||||||||:::|||||||||||||||||||||||||||:::|||||||||   :::|||
Db       3481 ACTGTGGCCCTCCACCCACCACCTCTGCCTGGAGCATACGTCCACCCAGCCTCCGAGGAG 3540

Qy       1181 Pro 1181
              |||
Db       3541 CCC 3543
```

```
RESULT 13
BC058397
LOCUS       BC058397                4402 bp    mRNA    linear   ROD 25-JUN-2004
DEFINITION  Mus musculus patched homolog 2, mRNA (cDNA clone IMAGE:6832070),
            partial cds.
ACCESSION   BC058397
VERSION     BC058397.1  GI:37231556
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4402)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4402)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 126 Row: o Column: 8
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6679516.
FEATURES             Location/Qualifiers
     source          1. .4402
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6832070"
                     /tissue_type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc"
                     /clone_lib="NIH_BMAP_FY0"
                     /lab_host="DH10B"
                     /note="Vector: pYX-ASC"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4402
Score:                    5589.50        Matches:         1084
Percent Similarity:       93.77%         Conservative:    44
Best Local Similarity:    90.11%         Mismatches:      72
Query Match:              89.12%         Indels:          4
DB:                       10             Gaps:            1

US-09-990-046-2 (1-1203) x BC058397 (1-4402)

Qy          1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
              |||  |||         |||  ||||||||||||||||||||||||||||||||||:::
Db        261 ATGGTTCGGCCACTGTCCCTTGGAGAGCTACCTCCCAGCTACACACCTCCAGCTCGGTCC 320

Qy         21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
              :::||||||  ||||||||||||||||||:::||||||||||||||||||||||||||||
Db        321 TCCGCACCTCATATCCTAGCTGGGAGCCTGCAGGCTCCTCTCTGGCTTCGAGCTTACTTC 380

Qy         41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
```


Db 381 CAAGGTCTACTCTTCTCCCTGGGGTGCAGGATCCAGAAACACTGCGGCAAAGTGCTCTTC 440
Qy 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db 441 CTGGGACTGGTGGCCTTTGGGGCTCTGGCACTGGGTCTCCGAGTGGCTGTAATTGAGACA 500
Qy 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 501 GACCTAGAACAGCTCTGGGTAGAAGTGGGCAGCAGGGTGAGCCAGGAGCTGCACTACACC 560
Qy 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 561 AAGGAGAAGCTGGGGGAAGAGGCTGCGTACACCTCCCAGATGTTGATTCAGACTGCGCAC 620
Qy 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db 621 CAGGAAGGGGGAAACGTCCTCACCCCCGAGGCACTTGACTTGCACCTCCAGGCGGCGCTC 680
Qy 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 681 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAATCCTGGGATTTGAACAAGATCTGC 740
Qy 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 741 TACAAATCAGGGGTTCCCCTTATTGAAAATGGGATGATCGAGCGGATGATTGAGAAGCTG 800
Qy 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 801 TTTCCCTGTGTGATCCTCACCCCGCTTGACTGCTTCTGGGAAGGAGCCAAACTCCAAGGG 860
Qy 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 861 GGCTCTGCCTACTTGCCGGGCCGCCCTGATATCCAGTGGACCAACCTGGACCCTCAGCAG 920
Qy 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 921 CTGCTCGAGGAGCTGGGCCCCTTTGCCTCTCTGGAGGGCTTCCGGGAACTGCTAGATAAG 980
Qy 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 981 GCACAGGTGGGCCAGGCCTATGTGGGGCGACCCTGTCTGGACCCTGATGACCCCCACTGT 1040
Qy 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1041 CCACCTAGTGCTCCCAACCGGCACAGCAGGCAGGCTCCCAATGTGGCTCAGGAGCTGAGT 1100
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 1101 GGGGGCTGCCATGGCTTCTCCCACAAGTTCATGCACTGGCAGGAGGAACTGCTACTAGGG 1160
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArg-AlaGluAlaLeuGlnSerThrPh 320
Db 1161 GGCACAGCCAGAGATCTCCAAGGACAGCTGCTGAGAGGCC------TTGCAGAGCACCTT 1214
Qy 320 eLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAs 340
Db 1215 CCTGCTCATGAGTCCCCGTCAGCTGTACGAGCACTTCCGGGGCGACTACCAGACACATGA 1274
Qy 340 pIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVa 360
Db 1275 CATCGGCTGGAGCGAGGAGCAGGCCAGCATGGTGCTGCAGGCCTGGCAGAGGCGCTTTGT 1334
Qy 360 lGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSe 380
Db 1335 GCAGCTAGCCCAGGAGGCTCTGCCGGCCAACGCGTCCCAGCAGATCCATGCCTTCTCCTC 1394
Qy 380 rThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGl 400
Db 1395 CACCACCCTGGATGACATCCTGCGCGCGTTCTCTGAAGTCAGCACCACCCGTGTGGTAGG 1454
Qy 400 yGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGl 420
Db 1455 AGGCTATCTGCTTATGCTGGCCTATGCCTGCGTAACAATGCTGCGGTGGGACTGCGCCCA 1514
Qy 420 nSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGl 440
Db 1515 GTCCCAGGGTGCCGTAGGTCTTGCTGGGGTGTTGCTGGTGGCCCTGGCGGTGGCCTCAGG 1574
Qy 440 yLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPr 460
Db 1575 TCTTGGGCTTTGTGCCCTACTTGGCATCACTTTCAATGCTGCCACTACACAGGTGCTGCC 1634
Qy 460 oPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGl 480
Db 1635 CTTCTTGGCTCTGGGCATTGGCGTGGATGACATCTTCCTGCTGGCGCATGCCTTCACAAA 1694
Qy 480 uAlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyTh 500
Db 1695 AGCCCCACCTGACACCCCTCTCCCAGAGCGTATGGGTGAGTGTTTGAGGAGCACGGGCAC 1754
Qy 500 rSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPr 520
Db 1755 CAGCGTGGCACTCACATCCGTCAACAACATGGTCGCCTTTTTCATGGCTGCCCTGGTTCC 1814
Qy 520 oIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVa 540
Db 1815 CATTCCTGCGCTGCGGGCCTTCTCCCTGCAGGCAGCCATAGTGGTCGGCTGCAACTTTGC 1874
Qy 540 lAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGl 560
Db 1875 AGCGGTAATGCTCGTCTTCCCTGCCATCCTCAGCCTCGACCTGCGCCGGCGCCACCGCCA 1934
Qy 560 nArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLe 580
Db 1935 ACGCCTGGACGTTCTCTGCTGCTTTTCTAGCCCCTGCTCCGCTCAGGTCATTCAGATGCT 1994
Qy 580 uProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVa 600
Db 1995 GCCCCAGGAGCTAGGGGACAGAGCAGTACCAGTGGGCATTGCCCACCTGACTGCCACCGT 2054
Qy 600 lGlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGl 620
Db 2055 GCAAGCCTTCACCCACTGCGAAGCCAGCAGCCAGCATGTAGTCACCATTTTGCCTCCTCA 2114
Qy 620 nAlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGl 640
Db 2115 AGCCCACCTGCTGTCTCCAGCTTCTGACCCACTGGGCTCCGAACTCTATAGCCCTGGAGG 2174
Qy 640 ySerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSe 660
Db 2175 GTCTACACGGGACCTTCTCAGTCAGGAGGAGGGGACAGGGCCACAGGCGGCCTGCAGGCC 2234
Qy 660 rLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLe 680
Db 2235 CCTGCTCTGTGCCCACTGGACTCTCGCCCATTTTGCCCGCTATCAGTTTGCACCTTTACT 2294
Qy 680 uLeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSe 700
Db 2295 GCTCCAGACACGAGCCAAGGCCCTGGTGTTGCTGTTCTTTGGGGCTCTTTTGGGCCTGAG 2354
Qy 700 rLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGl 720
Db 2355 CCTCTATGGAGCCACCTTGGTACAAGATGGGCTGGCCCTGACAGATGTGGTCCCTAGGGG 2414
Qy 720 yThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAl 740
Db 2415 CACCAAGGAACATGCTTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGC 2474
Qy 740 aLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHi 760
Db 2475 TCTAGTGACACAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCA 2534
Qy 760 sGlnArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgTh 780
Db 2535 CCAGCGCTTCAGCTCCCTCAAGGCTGTGCTGCCCCCACCTGCCACCCAGGCACCCCGCAC 2594

```
Qy        780 rTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTr 800
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       2595 CTGGCTTCACTACTACCGCAGCTGGCTACAGGGTATCCAGGCTGCATTTGACCAAGACTG 2654

Qy        800 pAlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAl 820
              |||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db       2655 GGCTTCTGGGCGCATCACCTGCCACTCTTACCGCAACGGCTCAGAAGATGGCGCCCTGGC 2714

Qy        820 aTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuTh 840
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       2715 CTACAAGCTGCTCATCCAAACCGGGAATGCCCAGGAGCCTCTGGATTTCAGCCAGCTGAC 2774

Qy        840 rThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLe 860
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db       2775 CACAAGGAAACTGGTGGACAAGGAGGGACTCATTCCCCCAGAGCTCTTCTACATGGGGCT 2834

Qy        860 uThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPr 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2835 AACCGTGTGGGTGAGCAGCGACCCCCTGGGCCTCGCAGCCTCTCAGGCCAACTTCTACCC 2894

Qy        880 oProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePr 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2895 CCCACCTCCAGAGTGGCTTCACGACAAATATGATACCACCGGGGAGAACCTTCGCATCCC 2954

Qy        900 oProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysTh 920
              |   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2955 GGCAGCCCAGCCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCATGGACTCCAGAAGAC 3014

Qy        920 rAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAl 940
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db       3015 TGCAGACTTTGTAGAAGCCATCGAAGGGGCCAGGGCGGCATGCACAGAGGCAGGCCAGGC 3074

Qy        940 aGlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLe 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3075 AGGGGTGCATGCCTACCCCAGTGGCTCCCCCTTCCTCTTCTGGGAGCAGTATCTGGGTCT 3134

Qy        960 uArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAl 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3135 TCGGCGCTGCTTCCTGCTGGCAGTCTGCATCTTGCTGGTGTGCACCTTCCTCGTCTGTGC 3194

Qy        980 aLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetTh 1000
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       3195 CCTGCTTCTACTCAGCCCGTGGACAGCTGGCCTCATAGTGCTGGTCCTGGCAATGATGAC 3254

Qy       1000 rValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVa 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3255 TGTGGAGCTCTTTGGTATCATGGGATTCCTGGGCATCAAACTGAGTGCCATCCCCGTGGT 3314

Qy       1020 lIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPh 1040
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       3315 AATCCTCGTGGCCTCTATAGGCATTGGTGTTGAATTCACAGTTCACGTGGCTCTGGGCTT 3374

Qy       1040 eLeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAl 1060
              |||||||:::   ||||||||||||||||||||||   |||||||||   ||||||||||
Db       3375 CCTGACCAGCCATGGTAGCCGGAACCTGCGGGCTGCTAGCGCTCTGGAACAGACCTTTGC 3434

Qy       1060 aProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHi 1080
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||::
Db       3435 CCCTGTGACTGATGGAGCTGTCTCCACCTTGCTGGGTCTGCTCATGCTTGCTGGTTCTAA 3494

Qy       1080 sPheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLe 1100
              :||||||||||||:::|||||||||||      ||||||||||||||||||||||||||||
Db       3495 CTTTGACTTCATCATAAGGTATTTCTTTGTGGTGCTGACGGTGCTGACACTCTTGGGCCT 3554

Qy       1100 uLeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVa 1120
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||:::||
Db       3555 GCTCCATGGACTCCTGCTGCTGCCTGTGCTGCTCTCTATCCTAGGCCCCCCGCCACAGGT 3614

Qy       1120 lIleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGl 1140
              |:::|||:::|||||||||||||||:::   |||:::     |||||||||   ||||||
Db       3615 GGTGCAGGTATACAAGGAGAGTCCACAGACCCTAAACTCCGCTGCTCCACAGAGAGGTGG 3674
```

```
Qy       1140 yLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMe 1160
              |||||||||            :::||||||||||||||||||||||||||||||||||||
Db       3675 GCTCAGGTGGGACAGGCCCCCCACCCTGCCCCAGAGTTTTGCCAGAGTGACTACCTCCAT 3734

Qy       1160 tThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGl 1180
              ||||||||||:::|||||||||||||||||||||||||:::|||||||||   :::||||
Db       3735 GACTGTGGCCCTCCACCCACCACCTCTGCCTGGAGCATACGTCCACCCAGCCTCCGAGGA 3794

Qy       1180 uProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPr 1200
              ||||      ||||||||||||      :::   |||||||||   ||||||   |||
Db       3795 GCCCACATAGTCTCCTGCTGCCGCCCCAGCAC--AACCTCAGTTGTAGAGGACTGGGTCT 3852

Qy       1200 oAlaThr 1202
              |||||||
Db       3853 AGCCACC 3859
```

```
RESULT 14
CQ717145
LOCUS       CQ717145               3195 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 3079 from Patent WO02068579.
ACCESSION   CQ717145
VERSION     CQ717145.1  GI:42278002
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 3079 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .3195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          3195
Score:                    5490.00        Matches:         1061
Percent Similarity:       99.81%         Conservative:    0
Best Local Similarity:    99.81%         Mismatches:      2
Query Match:              87.53%         Indels:          1
DB:                       6              Gaps:            0

US-09-990-046-2 (1-1203) x CQ717145 (1-3195)

Qy         24 GlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeu 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 CAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTCCAGGGCCTG 65

Qy         44 LeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeu 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTTCTGGGACTG 125

Qy         64 LeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGlu 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 TTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACAAACTTGGAA 185

Qy         84 GlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThrLysGluLys 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CAGCTCTGGGTAGAAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTACACCAAGGAGAAG 245

Qy        104 LeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGly 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGCCAGGAGGGA 305

Qy        124 GluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        306 GAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGCCCTCACTGCCAGT 365
Qy        144 LysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSer 163
Db        366 AAAGTCCAAGTATCACTCTATGGGAAGTCCTGGGATTTGAACAAAATCTGCTACAAGTCA 425
Qy        164 GlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeuProCys 183
Db        426 GGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTGTTTCCGTGC 485
Qy        184 ValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAla 203
Db        486 GTGATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGGGGCTCCGCC 545
Qy        204 TyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGlu 223
Db        546 TACCTGCCCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAGCTGCTGGAG 605
Qy        224 GluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnVal 243
Db        606 GAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAGGCACAGGTG 665
Qy        244 GlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCysProProSer 263
Db        666 GGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGCCCACCTAGT 725
Qy        264 AlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCys 283
Db        726 GCCCCCAACCATCACAGCAGGCAGGCTCCCAATGTGGCTCACGAGCTGAGTGGGGGCTGC 785
Qy        284 HisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAla 303
Db        786 CATGGCTTCTCCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGAGGCATGGCC 845
Qy        304 ArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMet 323
Db        846 AGAGACCCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTCTTGCTGATG 905
Qy        324 SerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAspIleGlyTrp 343
Db        906 AGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGACATTGGCTGG 965
Qy        344 SerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAla 363
Db        966 AGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTGCAGCTGGCC 1025
Qy        364 GlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeu 383
Db       1026 CAGGAGGCCCTGCCTGAGAACGCTTCCCAGCAGATCCATGCCTTCTCCTCCACCACCCTG 1085
Qy        384 AspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeu 403
Db       1086 GATGACATCCTGCATGCGTTCTCTGAAGTCAGTGCTGCCCGTGTGGTGGGAGGCTATCTG 1145
Qy        404 LeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGly 423
Db       1146 CTCATGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGT 1205
Qy        424 SerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeu 443
Db       1206 TCCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTC 1265
Qy        444 CysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAla 463
Db       1266 TGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCCTTCTTGGCT 1325
Qy        464 LeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuPro 483
Db       1326 CTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCATGCCTTCACAGAGGCTCTGCCT 1385
Qy        484 GlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValVal 503
Db       1386 GGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACCAGTGTCGTA 1445

Qy        504 LeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAla 523
Db       1446 CTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTTCCCATCCCTGCG 1505
Qy        524 LeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMet 543
Db       1506 CTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTTGTAGCCGTGATG 1565
Qy        544 LeuValProProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAsp 563
Db       1566 CTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGCCAGCGCCTTGAT 1625
Qy        564 ValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGlu 583
Db       1626 GTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAG 1685
Qy        584 LeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPhe 603
Db       1686 CTGGGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTT 1745
Qy        604 ThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeu 623
Db       1746 ACCCACTGTGAGGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTG 1805
Qy        624 ValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArg 643
Db       1806 GTGCCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGG 1865
Qy        644 AspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCys 663
Db       1866 GACCTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGT 1925
Qy        664 AlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSer 683
Db       1926 GCCCGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCA 1985
Qy        684 HisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGly 703
Db       1986 CATGCTAAGCC-ATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTCTACGGA 2044
Qy        704 AlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGlu 723
Db       2045 GCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACCAAGGAG 2104
Qy        724 HisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThr 743
Db       2105 CATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGGTGACC 2164
Qy        744 GlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPhe 763
Db       2165 CAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAGCGCTTC 2224
Qy        764 SerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHis 783
Db       2225 AGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGGCTGCAC 2284
Qy        784 TyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGly 803
Db       2285 TATTACCGCAACTGGCTACAGGGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGG 2344
Qy        804 ArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeu 823
Db       2345 CGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTG 2404
Qy        824 LeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLys 843
Db       2405 CTCATCCAGACTGGAGACGCCCAGGAGCCTCTGGATTTCAGCCAGCTGACCACAAGGAAG 2464
Qy        844 LeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrp 863
Db       2465 CTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTGACCGTGTGG 2524
```

```
Qy        864 ValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProPro 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2525 GTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCCCCACCTCCT 2584

Qy        884 GluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIleProProAlaGln 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2585 GAATGGCTGCACGACAAATACGACACCACGGGGGAGAACCTTCGCATCCCGCCAGCTCAG 2644

Qy        904 ProLeuGluPheAlaGlnProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 CCCTTGGAGTTTGCCCAGTTCCCCTTCCTGCTGCGTGGCCTCCAGAAGACTGCAGACTTT 2704

Qy        924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 GTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCAC 2764

Qy        944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2765 GCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCTGGGCCTGCGGCGCTGC 2824

Qy        964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2825 TTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGTCTGTGCTCTGCTGCTC 2884

Qy        984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2885 CTCAACCCCTGGACGGCTGGCCTCATAGTGCTGGTCCTGGCGATGATGACAGTGGAACTC 2944

Qy       1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2945 TTTGGTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTGATCCTTGTG 3004

Qy       1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3005 GCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCTGGGCTTCCTGACCACC 3064

Qy       1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3065 CAGGGCAGCCGGAACCTGCGGGCCGCCCATGCCCTTGAGCACACATTTGCCCCCGTGACC 3124

Qy       1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3125 GATGGGGCCATCTCCACATTGCTGGGTCTGCTCATGCTTGCTGGTTCCCACTTTGACTTC 3184

Qy       1084 IleValArg 1086
              |||||||||
Db       3185 ATTGTAAGG 3193
```

RESULT 15
BD227644

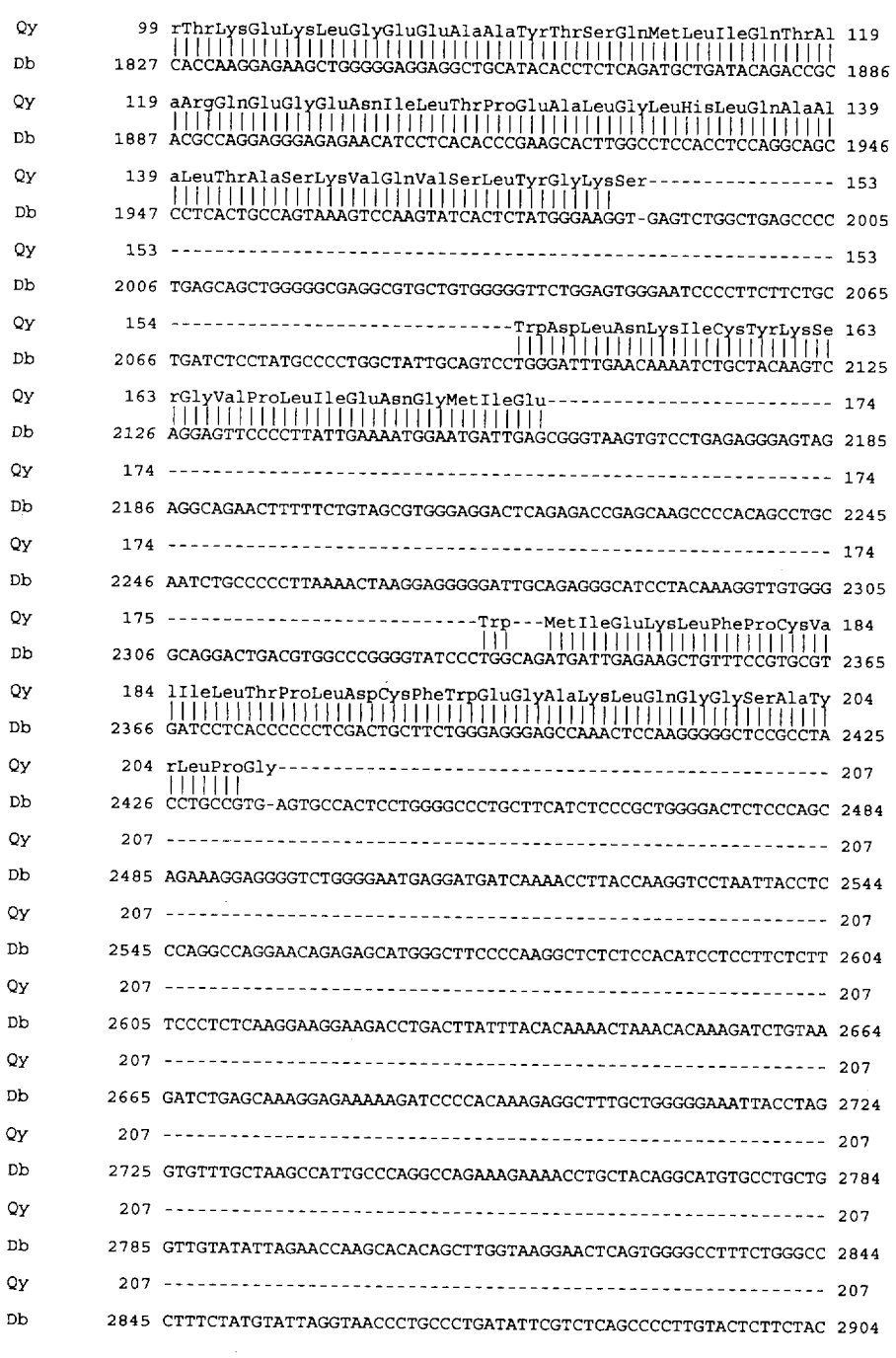
```
LOCUS       BD227644               12886 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel constitutional elements in hedgehog transmission pathway.
ACCESSION   BD227644
VERSION     BD227644.1  GI:33037414
KEYWORDS    JP 2002526050-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 12886)
  AUTHORS   Zaphiropoulos,P.G., Unden,A.B., Toftgard,R., Rahnama,F. and
            Hollingsworth,R.E.
  TITLE     Novel constitutional elements in hedgehog transmission pathway
  JOURNAL   Patent: JP 2002526050-A 4 20-AUG-2002;
            KAROLINSKA INNOVATIONS AB,PHARMACIA AND UPJOHN CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526050-A/4
            PD   20-AUG-2002
            PF   06-OCT-1999 JP 2000573395
            PR   06-OCT-1998 SE    9803393-9
            PI   PETER G ZAPHIROPOULOS,ANNE BIRGITTE UNDEN,RUNE TOFTGARD, PI
            FAHIMEH RAHNAMA,
            PI   ROBERT E HOLLINGSWORTH
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P25/16,A61P35/00,
            PC   C07K14/705,
            PC   C07K16/28,C12N5/10,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
             G01N33/53,
            PC   G01N33/58,G01N37/00,C12N15/00,A61K37/02,C12N5/00 CC   Novel
            constitutional elements in hedgehog transmission pathway FH   Key
                     Location/Qualifiers
            FT   source          1. .12886
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .12886
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

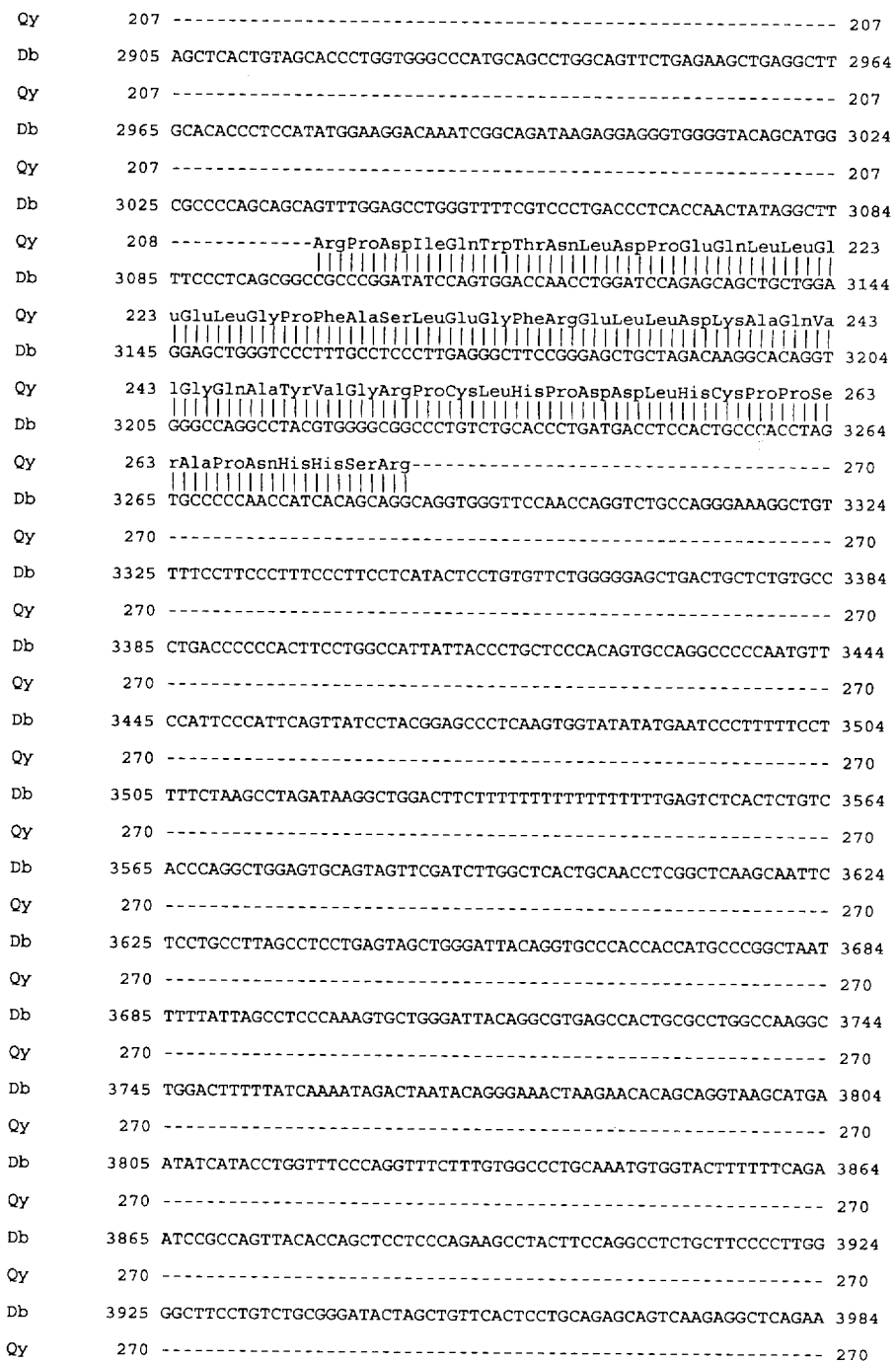
Alignment Scores:

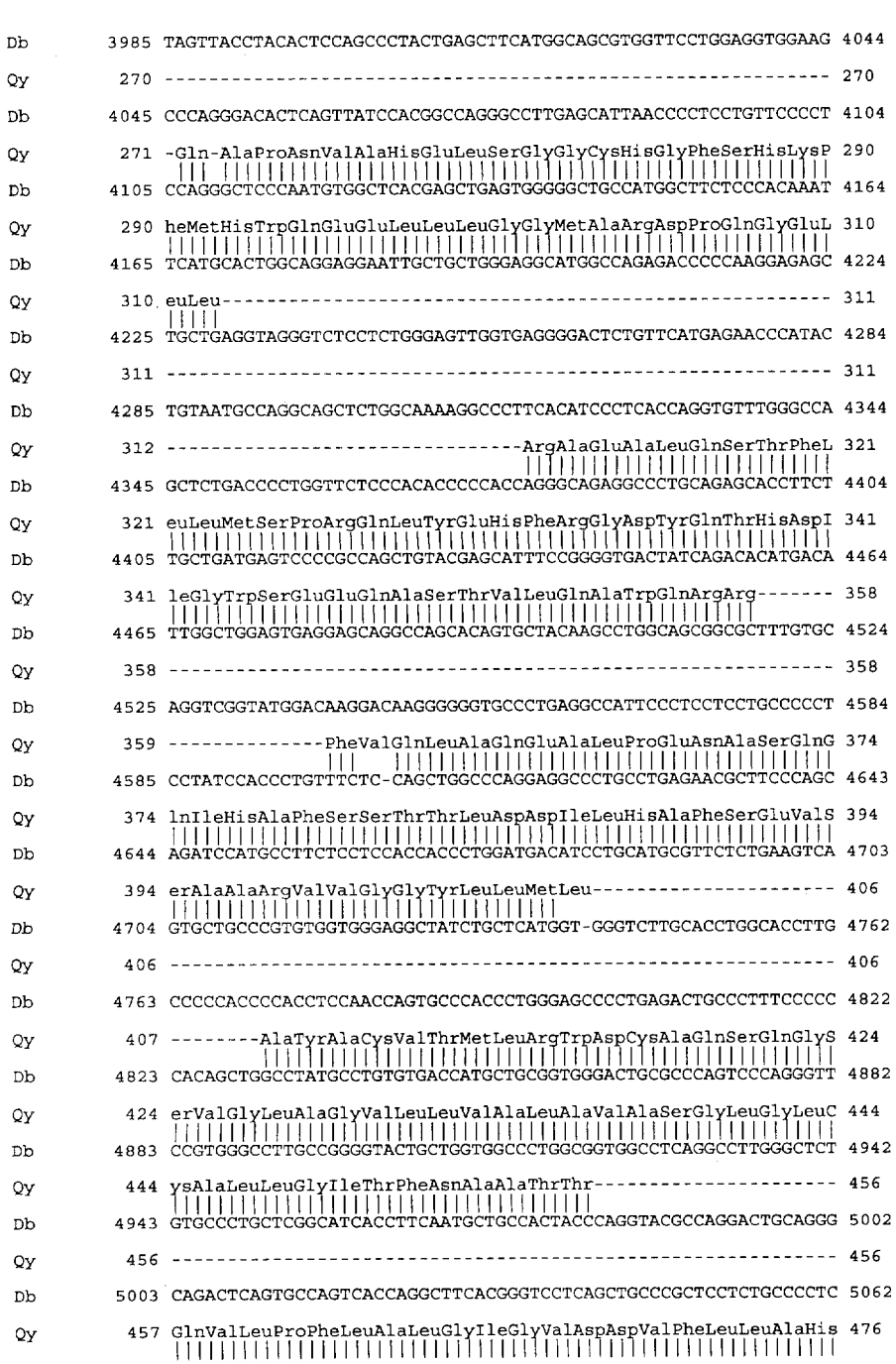
Pred. No.:	3.68e-291	Length:	12886
Score:	4682.50	Matches:	1166
Percent Similarity:	38.40%	Conservative:	1
Best Local Similarity:	38.37%	Mismatches:	13
Query Match:	74.66%	Indels:	1869
DB:	6	Gaps:	20

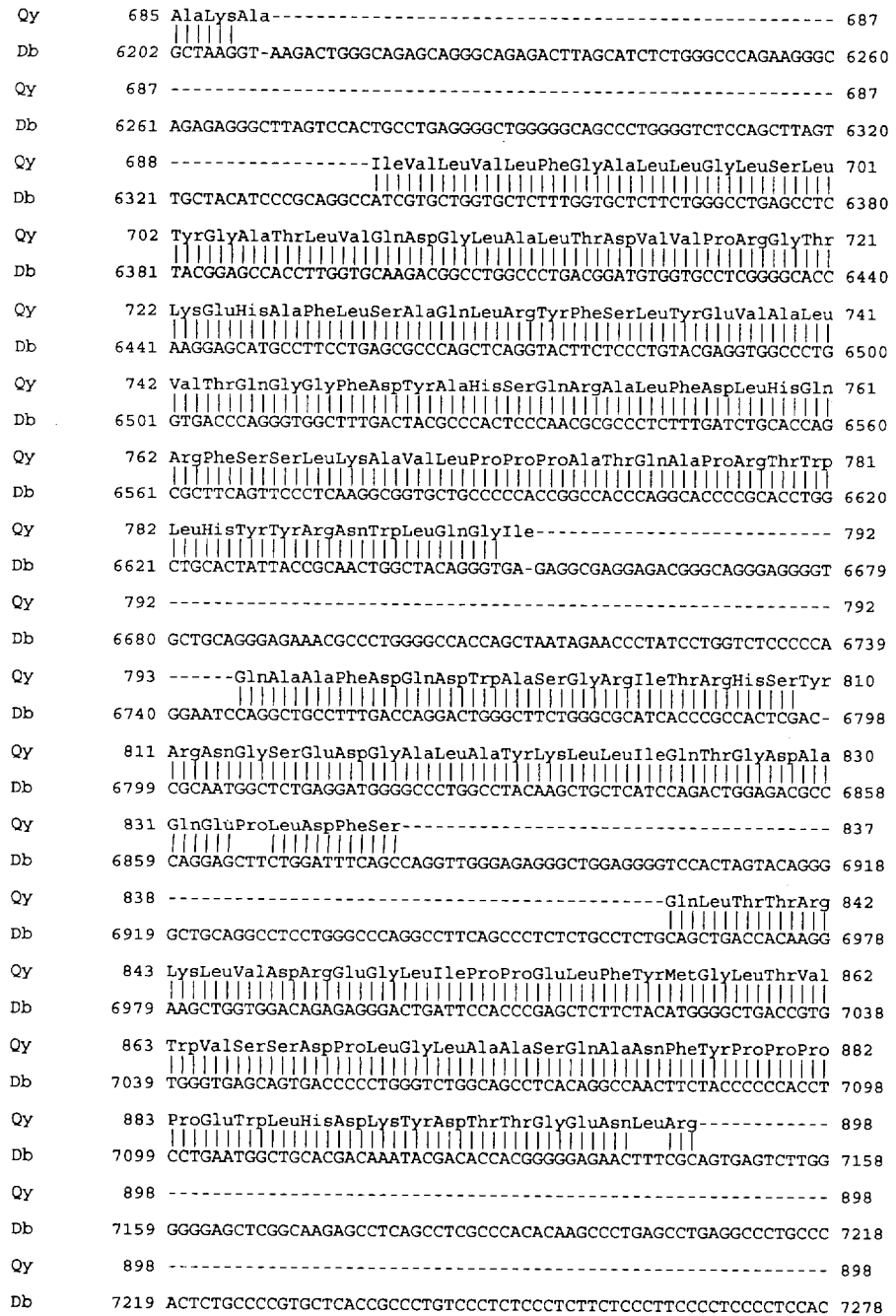
US-09-990-046-2 (1-1203) x BD227644 (1-12886)

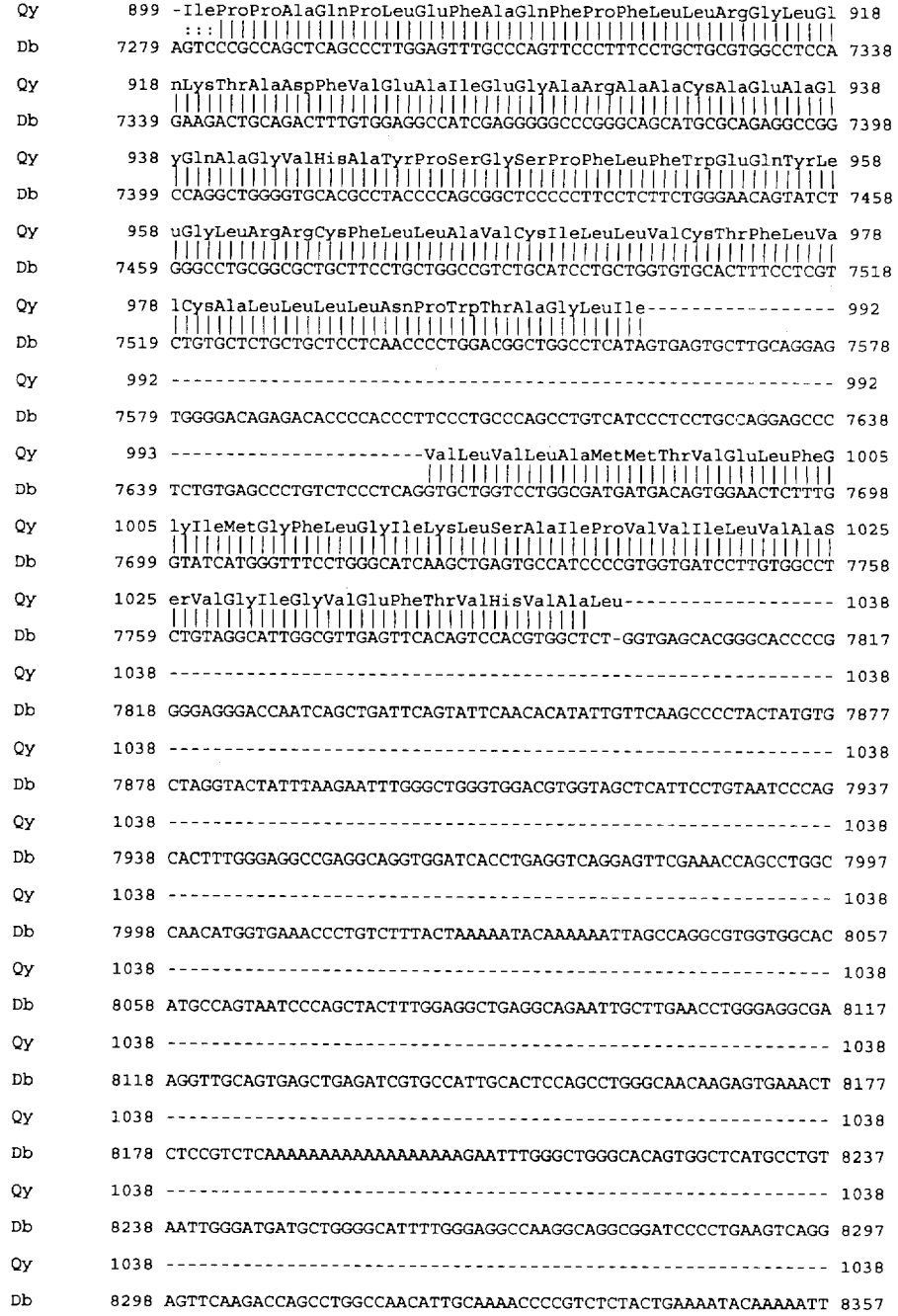
```
Qy         24 GlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeu 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 CAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTCCAGGGCCTG 1166

Qy         44 LeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeu 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 CTCTTCTCTCTGGGATGCGGGATCCAGAGACATTGTGGCAAAGTGCTCTTTCTGGGACTG 1226

Qy         64 LeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGlu 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 TTGGCCTTTGGGGCCCTGGCATTAGGTCTCCGCATGGCCATTATTGAGACAAACTTGGAA 1286

Qy         84 GlnLeuTrpValGlu---------------------------------------------- 88
              ||||||||||||||
Db       1287 CAGCTCTGGGTAGAAGGTAAGTTGTGGACACTGGCCATAGCTGCTCAGGTATGGTGAGCC 1346

Qy         88 ---------------------------------------------------------- 88

Db       1347 CAAGACAAGAACGGGGTGAGGAGCTGGCTACTGAGCTCTAGCAGGCCTGGCCCTGGGGCT 1406

Qy         88 ---------------------------------------------------------- 88

Db       1407 GGAGGGTCACCTGCTGGCCAGAGTCCTACACCTGGGCATCTAGGAACACCGTTCCCTCCC 1466

Qy         88 ---------------------------------------------------------- 88

Db       1467 ACAACCATAAATGGACATCTGCAGATGTTAGACCTTGTGAATTGGGTGTATAGAATATTT 1526

Qy         88 ---------------------------------------------------------- 88

Db       1527 GTCTGTGATTTTGCTTAAGCCCTAGACCACACAAGAAATCCGCAGAGCCACACAACCGAG 1586

Qy         88 ---------------------------------------------------------- 88

Db       1587 GCTTCTCCACTTCCCTGGCAGAGCTCCAGGACCCAGAAGCCTGGGGAGTCGGCCTGGGCC 1646

Qy         88 ---------------------------------------------------------- 88

Db       1647 ATGACCAGGCCCTCAGGGATAAGGCAGGGACTCCTCTCTGCCGCACCTCTCCCACTTGTC 1706

Qy         88 ---------------------------------------------------------- 88

Db       1707 TGGGGAGGCCTCAGAGTTAGAAGCCCCCTTCGCAAGTTCTGACCCGCCTAGGCCCTTTCC 1766

Qy         89 ----------------------------ValGlySerArgValSerGlnGluLeuHisTy 99
                                          ||||||||||||||||||||||||||||||
Db       1767 CCCCCAGCTTTCTCTGTTTGCTCTGGCAGTGGGCAGCCGGGTGAGCCAGGAGCTGCATTA 1826
```

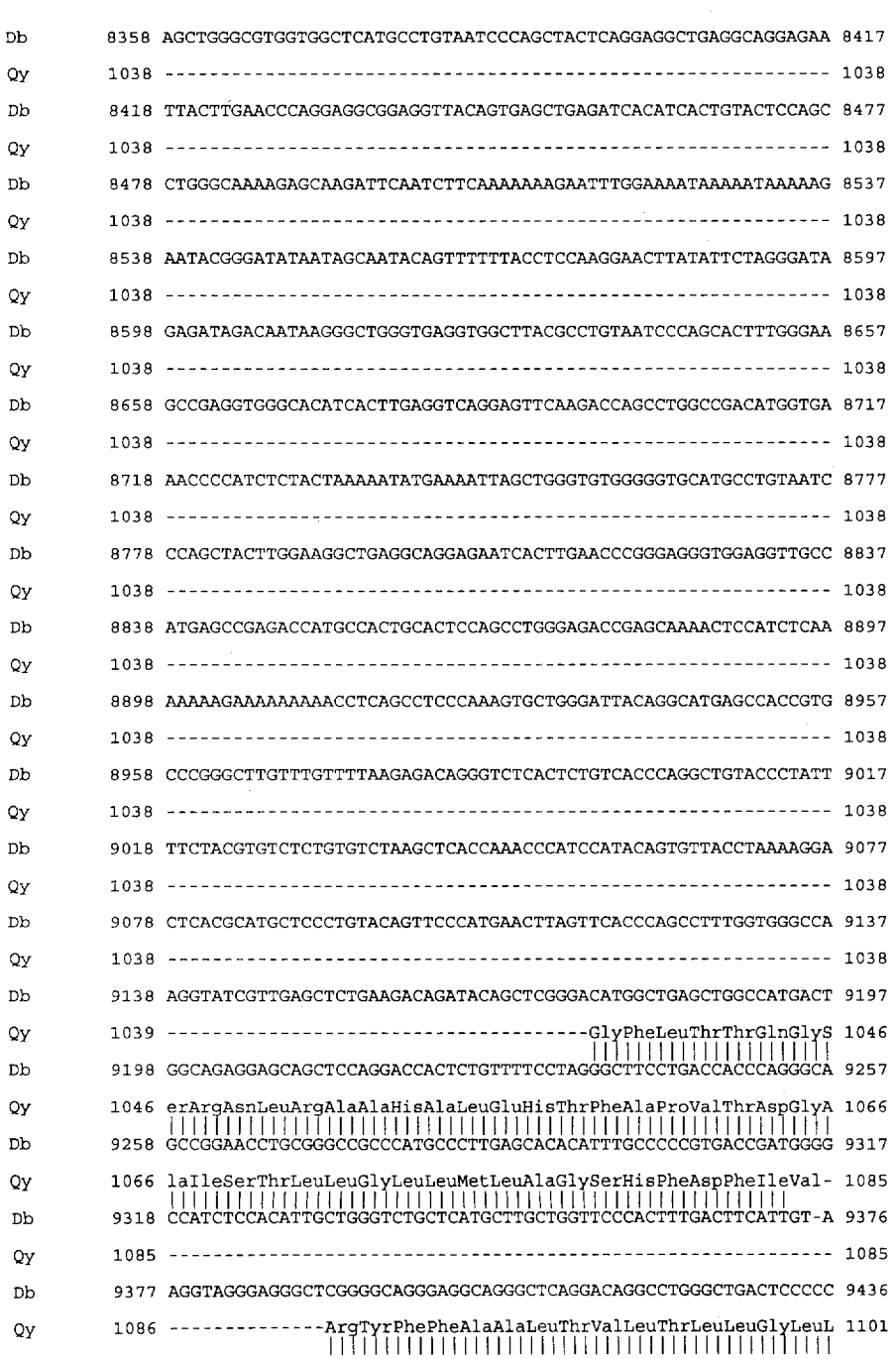

Qy 99 rThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAl 119
Db 1827 CACCAAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGC 1886
Qy 119 aArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAl 139
Db 1887 ACGCCAGGAGGGAGAGAACATCCTCACACCCGAAGCACTTGGCCTCCACCTCCAGGCAGC 1946
Qy 139 aLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSer---------- 153
Db 1947 CCTCACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGGT-GAGTCTGGCTGAGCCCC 2005
Qy 153 ---------- 153
Db 2006 TGAGCAGCTGGGGGCGAGGCGTGCTGTGGGGGTTCTGGAGTGGGAATCCCCTTCTTCTGC 2065
Qy 154 ----------TrpAspLeuAsnLysIleCysTyrLysSe 163
Db 2066 TGATCTCCTATGCCCCTGGCTATTGCAGTCCTGGGATTTGAACAAAATCTGCTACAAGTC 2125
Qy 163 rGlyValProLeuIleGluAsnGlyMetIleGlu---------- 174
Db 2126 AGGAGTTCCCCTTATTGAAAATGGAATGATTGAGCGGGTAAGTGTCCTGAGAGGGAGTAG 2185
Qy 174 ---------- 174
Db 2186 AGGCAGAACTTTTTCTGTAGCGTGGGAGGACTCAGAGACCGAGCAAGCCCCACAGCCTGC 2245
Qy 174 ---------- 174
Db 2246 AATCTGCCCCCTTAAAACTAAGGAGGGGGATTGCAGAGGGCATCCTACAAAGGTTGTGGG 2305
Qy 175 ----------Trp---MetIleGluLysLeuPheProCysVa 184
Db 2306 GCAGGACTGACGTGGCCCGGGGTATCCCTGGCAGATGATTGAGAAGCTGTTTCCGTGCGT 2365
Qy 184 lIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTy 204
Db 2366 GATCCTCACCCCCCTCGACTGCTTCTGGGAGGGAGCCAAACTCCAAGGGGGCTCCGCCTA 2425
Qy 204 rLeuProGly---------- 207
Db 2426 CCTGCCGTG-AGTGCCACTCCTGGGGCCCTGCTTCATCTCCCGCTGGGGACTCTCCCAGC 2484
Qy 207 ---------- 207
Db 2485 AGAAAGGAGGGGTCTGGGGAATGAGGATGATCAAAACCTTACCAAGGTCCTAATTACCTC 2544
Qy 207 ---------- 207
Db 2545 CCAGGCCAGGAACAGAGAGCATGGGCTTCCCCAAGGCTCTCTCCACATCCTCCTTCTCTT 2604
Qy 207 ---------- 207
Db 2605 TCCCTCTCAAGGAAGGAAGACCTGACTTATTTACACAAAACTAAACACAAAGATCTGTAA 2664
Qy 207 ---------- 207
Db 2665 GATCTGAGCAAAGGAGAAAAAGATCCCCACAAAGAGGCTTTGCTGGGGGAAATTACCTAG 2724
Qy 207 ---------- 207
Db 2725 GTGTTTGCTAAGCCATTGCCCAGGCCAGAAAGAAAACCTGCTACAGGCATGTGCCTGCTG 2784
Qy 207 ---------- 207
Db 2785 GTTGTATATTAGAACCAAGCACACAGCTTGGTAAGGAACTCAGTGGGGCCTTTCTGGGCC 2844
Qy 207 ---------- 207
Db 2845 CTTTCTATGTATTAGGTAACCCTGCCCTGATATTCGTCTCAGCCCCTTGTACTCTTCTAC 2904

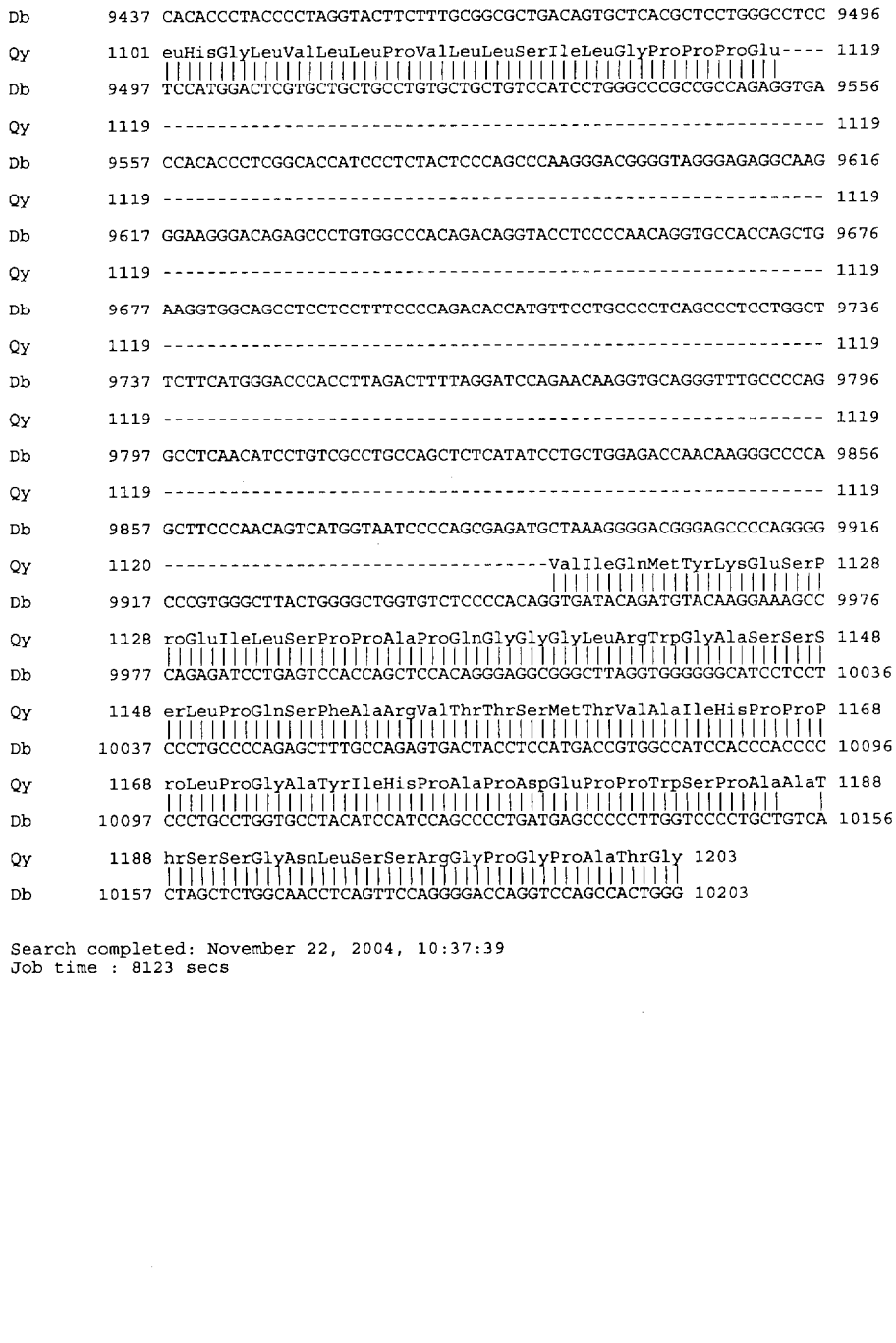

Qy 207 ---------- 207
Db 2905 AGCTCACTGTAGCACCCTGGTGGGCCCATGCAGCCTGGCAGTTCTGAGAAGCTGAGGCTT 2964
Qy 207 ---------- 207
Db 2965 GCACACCCTCCATATGGAAGGACAAATCGGCAGATAAGAGGAGGGTGGGGTACAGCATGG 3024
Qy 207 ---------- 207
Db 3025 CGCCCCAGCAGCAGTTTGGAGCCTGGGTTTTCGTCCCTGACCCTCACCAACTATAGGCTT 3084
Qy 208 ----------ArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGl 223
Db 3085 TTCCCTCAGCGGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAGCTGCTGGA 3144
Qy 223 uGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnVa 243
Db 3145 GGAGCTGGGTCCCTTTGCCTCCCTTGAGGGCTTCCGGGAGCTGCTAGACAAGGCACAGGT 3204
Qy 243 lGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCysProProSe 263
Db 3205 GGGCCAGGCCTACGTGGGGCGGCCCTGTCTGCACCCTGATGACCTCCACTGCCCACCTAG 3264
Qy 263 rAlaProAsnHisHisSerArg---------- 270
Db 3265 TGCCCCCAACCATCACAGCAGGCAGGTGGGTTCCAACCAGGTCTGCCAGGGAAAGGCTGT 3324
Qy 270 ---------- 270
Db 3325 TTTCCTTCCCTTTCCCTTCCTCATACTCCTGTGTTCTGGGGGAGCTGACTGCTCTGTGCC 3384
Qy 270 ---------- 270
Db 3385 CTGACCCCCCACTTCCTGGCCATTATTACCCTGCTCCCACAGTGCCAGGCCCCCAATGTT 3444
Qy 270 ---------- 270
Db 3445 CCATTCCCATTCAGTTATCCTACGGAGCCCTCAAGTGGTATATATGAATCCCTTTTTCCT 3504
Qy 270 ---------- 270
Db 3505 TTTCTAAGCCTAGATAAGGCTGGACTTCTTTTTTTTTTTTTTTTGAGTCTCACTCTGTC 3564
Qy 270 ---------- 270
Db 3565 ACCCAGGCTGGAGTGCAGTAGTTCGATCTTGGCTCACTGCAACCTCGGCTCAAGCAATTC 3624
Qy 270 ---------- 270
Db 3625 TCCTGCCTTAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCACCACCATGCCCGGCTAAT 3684
Qy 270 ---------- 270
Db 3685 TTTTATTAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGCCTGGCCAAGGC 3744
Qy 270 ---------- 270
Db 3745 TGGACTTTTTATCAAAATAGACTAATACAGGGAAACTAAGAACACAGCAGGTAAGCATGA 3804
Qy 270 ---------- 270
Db 3805 ATATCATACCTGGTTTCCCAGGTTTCTTTGTGGCCCTGCAAATGTGGTACTTTTTTCAGA 3864
Qy 270 ---------- 270
Db 3865 ATCCGCCAGTTACACCAGCTCCTCCCAGAAGCCTACTTCCAGGCCTCTGCTTCCCCTTGG 3924
Qy 270 ---------- 270
Db 3925 GGCTTCCTGTCTGCGGGATACTAGCTGTTCACTCCTGCAGAGCAGTCAAGAGGCTCAGAA 3984
Qy 270 ---------- 270


Db 3985 TAGTTACCTACACTCCAGCCCTACTGAGCTTCATGGCAGCGTGGTTCCTGGAGGTGGAAG 4044
Qy 270 ---------- 270
Db 4045 CCCAGGGACACTCAGTTATCCACGGCCAGGGCCTTGAGCATTAACCCCTCCTGTTCCCCT 4104
Qy 271 -Gln-AlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysP 290
Db 4105 CCAGGGCTCCCAATGTGGCTCACGAGCTGAGTGGGGGCTGCCATGGCTTCTCCCACAAAT 4164
Qy 290 heMetHisTrpGlnGluGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluL 310
Db 4165 TCATGCACTGGCAGGAGGAATTGCTGCTGGGAGGCATGGCCAGAGACCCCCAAGGAGAGC 4224
Qy 310 euLeu---------- 311
Db 4225 TGCTGAGGTAGGGTCTCCTCTGGGAGTTGGTGAGGGGACTCTGTTCATGAGAACCCATAC 4284
Qy 311 ---------- 311
Db 4285 TGTAATGCCAGGCAGCTCTGGCAAAAGGCCCTTCACATCCCTCACCAGGTGTTTGGGCCA 4344
Qy 312 ----------ArgAlaGluAlaLeuGlnSerThrPheL 321
Db 4345 GCTCTGACCCCTGGTTCTCCCACACCCCCACCAGGGCAGAGGCCCTGCAGAGCACCTTCT 4404
Qy 321 euLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAspI 341
Db 4405 TGCTGATGAGTCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGACA 4464
Qy 341 leGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArg------- 358
Db 4465 TTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGGCGCTTTGTGC 4524
Qy 358 ---------- 358
Db 4525 AGGTCGGTATGGACAAGGACAAGGGGGGTGCCCTGAGGCCATTCCCTCCTCCTGCCCCCT 4584
Qy 359 --------------PheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnG 374
Db 4585 CCTATCCACCCTGTTTCTC-CAGCTGGCCCAGGAGGCCCTGCCTGAGAACGCTTCCCAGC 4643
Qy 374 lnIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValS 394
Db 4644 AGATCCATGCCTTCTCCTCCACCACCCTGGATGACATCCTGCATGCGTTCTCTGAAGTCA 4703
Qy 394 erAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu---------- 406
Db 4704 GTGCTGCCCGTGTGGTGGGAGGCTATCTGCTCATGGT-GGGTCTTGCACCTGGCACCTTG 4762
Qy 406 ---------- 406
Db 4763 CCCCCACCCCACCTCCAACCAGTGCCCACCCTGGGAGCCCCTGAGACTGCCCTTTCCCCC 4822
Qy 407 --------AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlyS 424
Db 4823 CACAGCTGGCCTATGCCTGTGTGACCATGCTGCGGTGGGACTGCGCCCAGTCCCAGGGTT 4882
Qy 424 erValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuC 444
Db 4883 CCGTGGGCCTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCTCAGGCCTTGGGCTCT 4942
Qy 444 ysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr---------- 456
Db 4943 GTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGG 5002
Qy 456 ---------- 456
Db 5003 CAGACTCAGTGCCAGTCACCAGGCTTCACGGGTCCTCAGCTGCCCGCTCCTCTGCCCCTC 5062
Qy 457 GlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHis 476
Db 5063 CAGGTGCTGCCCTTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCCTGCTGGCGCAT 5122
Qy 477 AlaPheThrGluAlaLeuProGlyThrProLeu---------- 487
Db 5123 GCCTTCACAGAGGCTCTGCCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTC 5182
Qy 487 ---------- 487
Db 5183 ATCTGAGGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCCTTGGGCTGC 5242
Qy 487 ---------- 487
Db 5243 TAATGAACCTCGGTGCCTCTTGTCCCCATCTGTAAACAGGGGAAATAATAGTGCTGTGTC 5302
Qy 487 ---------- 487
Db 5303 CTAAGGGTTATTGTTTGGATCAGTGAGGTAACTCAAGTTGAATGCTTAGAACAGCCCATC 5362
Qy 487 ---------- 487
Db 5363 ATACGTACATGGTACCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCAC 5422
Qy 487 ---------- 487
Db 5423 CCCAAGTTCCTGAGCCTCCCCTTCACTCCACTTTGACACGGCCCCTCCCTTGTGACCTGA 5482
Qy 488 ----------GlnGluArgMetGlyGluCysLeuGlnArgThrGly 499
Db 5483 GGGCAGGTCCCCACTCTGTCCTGGCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGC 5542
Qy 500 ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuVal 519
Db 5543 ACCAGTGTCGTACTCACATCCATCAACAACATGGCCGCCTTCCTCATGGCTGCCCTCGTT 5602
Qy 520 ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe 539
Db 5603 CCCATCCCTGCGCTGCGAGCCTTCTCCCTACAGGCGGCCATAGTGGTTGGCTGCACCTTT 5662
Qy 540 ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCys 559
Db 5663 GTAGCCGTGATGCTTGTCTTCCCAGCCATCCTCAGCCTGGACCTACGGCGGCGCCACTGC 5722
Qy 560 GlnArgLeuAspValLeuCysCysPheSer---------- 569
Db 5723 CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCGTGCGCCCCAGCCCCTTCCT 5781
Qy 569 ---------- 569
Db 5782 CCCGTGACCCACGCCAGCCTGTCCCCTCACCAGCATTTCAAGGCACAGACCTGTCATCCA 5841
Qy 570 --------------SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 5842 CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 5901
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 5902 GGGGACGGGACAGTACCAGTGGGCATTGCCCACCTCACTGCCACAGTTCAAGCCTTTACC 5961
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 5962 CACTGTGAAGCCAGCAGCCAGCATGTGGTCACCATCCTGCCTCCCCAAGCCCACCTGGTG 6021
Qy 625 ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 6022 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 6081
Qy 645 LeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 6082 CTTCTAGGCCAGGAGGAGGAGACAAGGCAGAAGGCAGCCTGCAAGTCCCTGCCCTGTGCC 6141
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 6142 CGCTGGAATCTTGCCCATTTCGCCCGCTATCAGTTTGCCCCGTTGCTGCTCCAGTCACAT 6201


Qy 685 AlaLysAla 687
Db 6202 GCTAAGGT-AAGACTGGGCAGAGCAGGGCAGAGACTTAGCATCTCTGGGCCCAGAAGGGC 6260
Qy 687 687
Db 6261 AGAGAGGGCTTAGTCCACTGCCTGAGGGGCTGGGGGCAGCCCTGGGGTCTCCAGCTTAGT 6320
Qy 688 IleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeu 701
Db 6321 TGCTACATCCCGCAGGCCATCGTGCTGGTGCTCTTTGGTGCTCTTCTGGGCCTGAGCCTC 6380
Qy 702 TyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThr 721
Db 6381 TACGGAGCCACCTTGGTGCAAGACGGCCTGGCCCTGACGGATGTGGTGCCTCGGGGCACC 6440
Qy 722 LysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeu 741
Db 6441 AAGGAGCATGCCTTCCTGAGCGCCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTG 6500
Qy 742 ValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGln 761
Db 6501 GTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGCACCAG 6560
Qy 762 ArgPheSerSerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrp 781
Db 6561 CGCTTCAGTTCCCTCAAGGCGGTGCTGCCCCCACCGGCCACCCAGGCACCCCGCACCTGG 6620
Qy 782 LeuHisTyrTyrArgAsnTrpLeuGlnGlyIle 792
Db 6621 CTGCACTATTACCGCAACTGGCTACAGGGTGA-GAGGCGAGGAGACGGGCAGGGAGGGGT 6679
Qy 792 792
Db 6680 GCTGCAGGGAGAAACGCCCTGGGGCCACCAGCTAATAGAACCCTATCCTGGTCTCCCCCA 6739
Qy 793 GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyr 810
Db 6740 GGAATCCAGGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGCATCACCCGCCACTCGAC- 6798
Qy 811 ArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAla 830
Db 6799 CGCAATGGCTCTGAGGATGGGGCCCTGGCCTACAAGCTGCTCATCCAGACTGGAGACGCC 6858
Qy 831 GlnGluProLeuAspPheSer 837
Db 6859 CAGGAGCTTCTGGATTTCAGCCAGGTTGGGAGAGGGCTGGAGGGGTCCACTAGTACAGGG 6918
Qy 838 GlnLeuThrThrArg 842
Db 6919 GCTGCAGGCCTCCTGGGCCCAGGCCTTCAGCCCTCTCTGCCTCTGCAGCTGACCACAAGG 6978
Qy 843 LysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrVal 862
Db 6979 AAGCTGGTGGACAGAGAGGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTGACCGTG 7038
Qy 863 TrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProPro 882
Db 7039 TGGGTGAGCAGTGACCCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCCCCACCT 7098
Qy 883 ProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArg 898
Db 7099 CCTGAATGGCTGCACGACAAATACGACACCACGGGGGAGAACTTTCGCAGTGAGTCTTGG 7158
Qy 898 898
Db 7159 GGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCACACAAGCCCTGAGCCTGAGGCCCTGCCC 7218
Qy 898 898
Db 7219 ACTCTGCCCCGTGCTCACCGCCCTGTCCCTCTCCCTCTTCTCCCTTCCCCTCCCCTCCAC 7278


Qy 899 IleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGl 918
Db 7279 AGTCCCGCCAGCTCAGCCCTTGGAGTTTGCCCAGTTCCCTTTCCTGCTGCGTGGCCTCCA 7338
Qy 918 nLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGl 938
Db 7339 GAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGGCCGG 7398
Qy 938 yGlnAlaGlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLe 958
Db 7399 CCAGGCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACAGTATCT 7458
Qy 958 uGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuVa 978
Db 7459 GGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGCACTTTCCTCGT 7518
Qy 978 lCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIle 992
Db 7519 CTGTGCTCTGCTGCTCCTCAACCCCTGGACGGCTGGCCTCATAGTGAGTGCTTGCAGGAG 7578
Qy 992 992
Db 7579 TGGGGACAGAGACACCCCACCCTTCCCTGCCCAGCCTGTCATCCCTCCTGCCAGGAGCCC 7638
Qy 993 ValLeuValLeuAlaMetMetThrValGluLeuPheG 1005
Db 7639 TCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTG 7698
Qy 1005 lyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaS 1025
Db 7699 GTATCATGGGTTTCCTGGGCATCAAGCTGAGTGCCATCCCCGTGGTGATCCTTGTGGCCT 7758
Qy 1025 erValGlyIleGlyValGluPheThrValHisValAlaLeu 1038
Db 7759 CTGTAGGCATTGGCGTTGAGTTCACAGTCCACGTGGCTCT-GGTGAGCACGGGCACCCCG 7817
Qy 1038 1038
Db 7818 GGGAGGGACCAATCAGCTGATTCAGTATTCAACACATATTGTTCAAGCCCCTACTATGTG 7877
Qy 1038 1038
Db 7878 CTAGGTACTATTTAAGAATTTGGGCTGGGTGGACGTGGTAGCTCATTCCTGTAATCCCAG 7937
Qy 1038 1038
Db 7938 CACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGTTCGAAACCAGCCTGGC 7997
Qy 1038 1038
Db 7998 CAACATGGTGAAACCCTGTCTTTACTAAAAATACAAAAAATTAGCCAGGCGTGGTGGCAC 8057
Qy 1038 1038
Db 8058 ATGCCAGTAATCCCAGCTACTTTGGAGGCTGAGGCAGAATTGCTTGAACCTGGGAGGCGA 8117
Qy 1038 1038
Db 8118 AGGTTGCAGTGAGCTGAGATCGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACT 8177
Qy 1038 1038
Db 8178 CTCCGTCTCAAAAAAAAAAAAAAAAAAGAATTTGGGCTGGGCACAGTGGCTCATGCCTGT 8237
Qy 1038 1038
Db 8238 AATTGGGATGATGCTGGGGCATTTTGGGAGGCCAAGGCAGGCGGATCCCCTGAAGTCAGG 8297
Qy 1038 1038
Db 8298 AGTTCAAGACCAGCCTGGCCAACATTGCAAAACCCCGTCTCTACTGAAAATACAAAAATT 8357
Qy 1038 1038





Search completed: November 22, 2004, 10:37:39
Job time : 8123 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 22, 2004, 06:48:29 ; Search time 93 Seconds
(without alignments)
7442.749 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	1203	2	AAQ89375	Aaq89375 homo sapi
2	6272	100.0	1211	2	Q6UX14	Q6ux14 homo sapien
3	6272	100.0	1211	2	AAQ88919	Aaq88919 homo sapi
4	6258	99.8	1203	1	PTC2_HUMAN	Q9y6c5 homo sapien
5	5599	89.3	1182	1	PTC2_MOUSE	O35595 mus musculu
6	5599	89.3	1182	2	CAC88120	Cac88120 mus muscu
7	4119	65.7	1413	2	Q9DEF3	Q9def3 xenopus lae
8	4106	65.5	1422	2	Q6IRA5	Q6ira5 xenopus lae
9	4106	65.5	1422	2	AAH70995	Aah70995 xenopus l
10	4042.5	64.5	1220	1	PTC1_BRARE	Q98864 brachydanio
11	3348	53.4	1447	1	PTC1_HUMAN	Q13635 homo sapien
12	3344	53.3	913	2	Q90XB9	Q90xb9 gallus gall
13	3340	53.3	1442	1	PTC1_CHICK	Q90693 gallus gall
14	3339.5	53.2	1434	2	Q6UY90	Q6uy90 rattus norv
15	3339.5	53.2	1434	2	AAQ67738	Aaq67738 rattus no
16	3337	53.2	1434	1	PTC1_MOUSE	Q61115 mus musculu
17	3308	52.7	1239	2	Q9DEF4	Q9def4 xenopus lae
18	3308	52.7	1418	2	Q98SW6	Q98sw6 xenopus lae
19	3253	51.9	1243	2	Q9W6T6	Q9w6t6 brachydanio
20	2242	35.7	1318	2	Q9XYP5	Q9xyp5 junonia coe
21	2025.5	32.3	1157	2	Q7Q2Y4	Q7q2y4 anopheles g
22	1992	31.8	1286	1	PATC_DROME	P18502 drosophila
23	1812	28.9	651	2	Q6TKP9	Q6tkp9 homo sapien
24	1812	28.9	651	2	AAR21239	Aar21239 homo sapi
25	1776.5	28.3	608	2	Q9Z2A1	Q9z2a1 rattus norv
26	1708.5	27.2	1405	1	PTC1_CAEEL	Q09614 caenorhabdi
27	1625	25.9	1388	2	Q9N4A1	Q9n4a1 caenorhabdi
28	1623.5	25.9	1391	2	Q95Y30	Q95y30 caenorhabdi
29	992	15.8	714	2	Q09540	Q09540 caenorhabdi
30	984	15.7	255	1	PTC2_CYNPY	O42334 cynops pyrr
31	866.5	13.8	287	2	Q9DDZ0	Q9ddz0 xenopus lae
32	797	12.7	257	1	PTC1_CYNPY	O42335 cynops pyrr
33	769	12.3	234	2	Q8MKB3	Q8mkb3 equus cabal
34	640	10.2	1278	1	NPC1_HUMAN	O15118 homo sapien
35	635	10.1	1277	1	NPC1_PIG	P56941 sus scrofa
36	633	10.1	1361	2	Q7XUB7	Q7xub7 oryza sativ
37	622	9.9	1276	2	Q8MI49	Q8mi49 felis silve
38	619.5	9.9	1286	2	Q9TT75	Q9tt75 oryctolagus
39	618	9.9	1276	2	Q8MKD8	Q8mkd8 felis silve
40	612	9.8	1276	2	Q9N0Q0	Q9n0q0 felis silve
41	611.5	9.7	1277	2	Q9GLC9	Q9glc9 bos taurus
42	609.5	9.7	1276	2	Q9GK52	Q9gk52 canis famil
43	604.5	9.6	1277	2	Q9JLG3	Q9jlg3 cricetulus
44	602.5	9.6	1278	1	NPC1_MOUSE	O35604 mus musculu
45	600.5	9.6	1359	2	Q9UHC9	Q9uhc9 homo sapien

ALIGNMENTS

RESULT 1
AAQ89375
ID AAQ89375 PRELIMINARY; PRT; 1203 AA.
AC AAQ89375;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Patched 2.
GN UNQ560.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY359016; AAQ89375.1; -.
SQ SEQUENCE 1203 AA; 130573 MW; FFFA069997EEB6EB CRC64;

Query Match 100.0%; Score 6272; DB 2; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203

Db       1201 ATG 1203


RESULT 2
Q6UX14
ID   Q6UX14      PRELIMINARY;      PRT;  1211 AA.
AC   Q6UX14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Patched 2.
GN   ORFNames=UNQ560;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358555; AAQ88919.1; -.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
SQ   SEQUENCE   1211 AA;  131568 MW;  303D4FC55D39FB77 CRC64;

  Query Match           100.0%;  Score 6272;  DB 2;  Length 1211;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
```

```
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203

Db       1201 ATG 1203
```

```
RESULT 3
AAQ88919
ID   AAQ88919    PRELIMINARY;      PRT;  1211 AA.
AC   AAQ88919;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Patched 2.
GN   UNQ560.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT   Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT   Bioinformatics Assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358555; AAQ88919.1; -.
SQ   SEQUENCE   1211 AA;  131568 MW;  303D4FC55D39FB77 CRC64;
```

```
  Query Match           100.0%;  Score 6272;  DB 2;  Length 1211;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
```

```
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

```
RESULT 4
PTC2_HUMAN
ID   PTC2_HUMAN     STANDARD;      PRT;  1203 AA.
AC   Q9Y6C5; O95341; O95856;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Patched protein homolog 2 (PTC2).
GN   Name=PTCH2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99030620; PubMed=9811851;
RA   Carpenter D., Stone D.M., Brush J., Ryan A., Armanini M., Frantz G.,
RA   Rosenthal A., de Sauvage F.J.;
RT   "Characterization of two patched receptors for the vertebrate hedgehog
RT   protein family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:13630-13634(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND INVOLVEMENT IN MDB AND BCC.
RX   MEDLINE=99135908; PubMed=9931336;
RA   Smyth I., Narang M.A., Evans T., Heimann C., Nakamura Y.,
RA   Chenevix-Trench G., Pietsch T., Wicking C., Wainwright B.J.;
RT   "Isolation and characterization of human patched 2 (PTCH2), a putative
RT   tumour suppressor gene in basal cell carcinoma and medulloblastoma on
RT   chromosome 1p32.";
RL   Hum. Mol. Genet. 8:291-297(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=99151521; PubMed=10029063;
RA   Zaphiropoulos P.G., Unden A.B., Rahnama F., Hollingsworth R.E.,
RA   Toftgard R.;
RT   "PTCH2, a novel human patched gene, undergoing alternative splicing
RT   and up-regulated in basal cell carcinomas.";
RL   Cancer Res. 59:787-792(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GLN-346; LYS-493;
RP   TYR-622; MET-988; MET-1019 AND MET-1121.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May have a role in epidermal development. May act as a
CC       receptor for Sonic hedgehog (SHH).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q9Y6C5-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9Y6C5-2; Sequence=VSP_004542;
CC   -!- DISEASE: Defects in PTCH2 are a cause of medulloblastoma (MDB)
CC       [MIM:155255]. MDB is a malignant, invasive embryonal tumor of the
CC       cerebellum with a preferential manifestation in children. Although
CC       the majority of medulloblastomas occur sporadically, some manifest
CC       within familial cancer syndromes such as Turcot syndrome and basal
CC       cell nevus syndrome (Gorlin syndrome).
CC   -!- DISEASE: Defects in PTCH2 are a cause of sporadic basal cell
CC       carcinoma (BCC) [MIM:605462].
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF091501; AAC79847.1; -.
DR   EMBL; AF087651; AAD25953.1; -.
DR   EMBL; AF119569; AAD17260.1; -.
DR   EMBL; AY438664; AAR05447.1; -.
DR   Genew; HGNC:9586; PTCH2.
DR   MIM; 603673; -.
DR   MIM; 155255; -.
DR   MIM; 605462; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   GO; GO:0008544; P:epidermal differentiation; TAS.
DR   GO; GO:0006461; P:protein complex assembly; TAS.
DR   GO; GO:0007283; P:spermatogenesis; TAS.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Alternative splicing; Glycoprotein; Receptor; Transmembrane.
FT   DOMAIN       1    57       Cytoplasmic (Potential).
FT   TRANSMEM    58    78       Potential.
FT   DOMAIN      79   392       Extracellular (Potential).
FT   TRANSMEM   393   413       Potential.
FT   DOMAIN     414   428       Cytoplasmic (Potential).
FT   TRANSMEM   429   449       Potential.
FT   DOMAIN     450   457       Extracellular (Potential).
FT   TRANSMEM   458   478       Potential.
FT   DOMAIN     479   501       Cytoplasmic (Potential).
FT   TRANSMEM   502   522       Potential.
FT   DOMAIN     523   531       Extracellular (Potential).
FT   TRANSMEM   532   552       Potential.
FT   DOMAIN     553   686       Cytoplasmic (Potential).
FT   TRANSMEM   687   707       Potential.
FT   DOMAIN     708   963       Extracellular (Potential).
FT   TRANSMEM   964   984       Potential.
FT   DOMAIN     985   991       Cytoplasmic (Potential).
FT   TRANSMEM   992  1012       Potential.
FT   DOMAIN    1013  1013       Extracellular (Potential).
FT   TRANSMEM  1014  1034       Potential.
FT   DOMAIN    1035  1064       Cytoplasmic (Potential).
FT   TRANSMEM  1065  1085       Potential.
FT   DOMAIN    1086  1093       Extracellular (Potential).
FT   TRANSMEM  1094  1114       Potential.
FT   DOMAIN    1115  1203       Cytoplasmic (Potential).
FT   DOMAIN     394   552       SSD.
FT   CARBOHYD   370   370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   812   812       N-linked (GlcNAc. . .) (Potential).
```

```
FT   VARSPLIC   1143   1203       WGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPW
FT                                SPAATSSGNLSSRGPGPATG -> PEEI (in isoform
FT                                2).
FT                                /FTId=VSP_004542.
FT   VARIANT     346    346       E -> Q.
FT                                /FTId=VAR_018935.
FT   VARIANT     493    493       E -> K.
FT                                /FTId=VAR_018936.
FT   VARIANT     622    622       H -> Y.
FT                                /FTId=VAR_018937.
FT   VARIANT     988    988       T -> M.
FT                                /FTId=VAR_018938.
FT   VARIANT    1019   1019       V -> M.
FT                                /FTId=VAR_018939.
FT   VARIANT    1121   1121       I -> M.
FT                                /FTId=VAR_018940.
FT   CONFLICT      2      2       T -> N (in Ref. 2).
FT   CONFLICT    120    120       R -> L (in Ref. 2).
FT   CONFLICT    175    175       R -> W (in Ref. 1).
FT   CONFLICT    753    753       Q -> R (in Ref. 2).
FT   CONFLICT    787    787       N -> S (in Ref. 2).
FT   CONFLICT    833    833       P -> L (in Ref. 3).
FT   CONFLICT    837    837       S -> G (in Ref. 2).
FT   CONFLICT    846    846       D -> E (in Ref. 2).
FT   CONFLICT    897    897       L -> F (in Ref. 3).
SQ   SEQUENCE   1203 AA;  130543 MW;  4FAB06999782C031 CRC64;
```

Query Match 99.8%; Score 6258; DB 1; Length 1203;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

RESULT 5

```
PTC2_MOUSE
ID   PTC2_MOUSE     STANDARD;      PRT;  1182 AA.
AC   O35595;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Patched protein homolog 2 (PTC2).
GN   Name=Ptch2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=98122566; PubMed=9462734;
RA   Motoyama J., Takabatake T., Takeshima K., Hui C.-C.;
RT   "Ptch2, a second mouse Patched gene is co-expressed with Sonic
RT   hedgehog.";
RL   Nat. Genet. 18:104-106(1998).
RN   [2]
RP   SEQUENCE OF 196-446 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Neuroretina;
RX   MEDLINE=97379366; PubMed=9237688;
RA   Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,
RA   Takeshima K.;
RT   "Hedgehog and patched gene expression in adult ocular tissues.";
RL   FEBS Lett. 410:485-489(1997).
CC   -!- FUNCTION: May have a role in epidermal development. May act as a
```

```
CC       receptor for Sonic hedgehog (SHH).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in epithelial cells of the
CC       developing hair, tooth and whisker.
CC   -!- DEVELOPMENTAL STAGE: Detected in 8.5 to 17.5 dpc embryos.
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB010833; BAA24691.1; -.
DR   PIR; T13952; T13952.
DR   MGD; MGI:1095405; Ptch2.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Glycoprotein; Receptor; Transmembrane.
FT   DOMAIN       1     57       Cytoplasmic (Potential).
FT   TRANSMEM     58    78       Potential.
FT   DOMAIN       79    394      Extracellular (Potential).
FT   TRANSMEM     395   414      Potential.
FT   DOMAIN       415   428      Cytoplasmic (Potential).
FT   TRANSMEM     429   449      Potential.
FT   DOMAIN       450   457      Extracellular (Potential).
FT   TRANSMEM     458   478      Potential.
FT   DOMAIN       479   501      Cytoplasmic (Potential).
FT   TRANSMEM     502   522      Potential.
FT   DOMAIN       523   531      Extracellular (Potential).
FT   TRANSMEM     532   552      Potential.
FT   DOMAIN       553   686      Cytoplasmic (Potential).
FT   TRANSMEM     687   707      Potential.
FT   DOMAIN       708   963      Extracellular (Potential).
FT   TRANSMEM     964   984      Potential.
FT   DOMAIN       985   991      Cytoplasmic (Potential).
FT   TRANSMEM     992   1012     Potential.
FT   DOMAIN       1013  1013     Extracellular (Potential).
FT   TRANSMEM     1014  1034     Potential.
FT   DOMAIN       1035  1064     Cytoplasmic (Potential).
FT   TRANSMEM     1065  1085     Potential.
FT   DOMAIN       1086  1086     Extracellular (Potential).
FT   TRANSMEM     1087  1107     Potential.
FT   DOMAIN       1108  1182     Cytoplasmic (Potential).
FT   DOMAIN       394   552      SSD.
FT   CARBOHYD     370   370      N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     812   812      N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1182 AA;  128585 MW;  715233D912C352F2 CRC64;

  Query Match           89.3%;  Score 5599;  DB 1;  Length 1182;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 1074;  Conservative   43;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              | |    | ||||||||||::|| ||||||:|||||||||||||||| ||:|||||||
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              |||:|||||||||:|:|||:|||||||||||||||||||||||||||||||||||||||
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||| |:|||||| |||||||||||||||||||||||||||||||||||||||| |||||
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        181 FPCVILTPLDLCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              |||||||||||| ||| |||||||| |||||||| ||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              | ||| ||:|||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              |||||||| |||||||||||||||||| |||||  ||||||||||||||||||||||||
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              | | ||| |||||||: ||||| |||:||| || |||||||||||||||||||||| |
Db        481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              |||||||||||||||||| ||||||||||||||||||:||||||  |||||||||||
Db        541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              |||||||||||||||||||: | ||||||||:|||||||||| ||| |  :|||:
Db        601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              | || | |||||||||||||||: |||:||: ||||||||||||||||||||||||||
Db        661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||:|||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              |||||||||||| ||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              |||||:|||||||||||||: |||||||| ||| |||||||:||||||||||||:
Db       1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||:|||| ||||||||||||:|||||||||||||:|:|:|||||: |:  ||| ||
Db       1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
              |||    :|||||||||||||:|||||||||:||| :||
Db       1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181


RESULT 6
CAC88120
ID   CAC88120    PRELIMINARY;      PRT;  1182 AA.
AC   CAC88120;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
```

```
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Patched 2 protein.
GN   PTCH2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129 SvJ; TISSUE=Liver;
RA   Froehlich L., Zhanquin L., Beier D.R., Lanske B.;
RT   "Genomic structure and refined chromosomal localization of the mouse
RT   ptch2 gene.";
RL   Cytogenet. Genome Res. 97:106-110(2002).
DR   EMBL; AJ133482; CAC88120.1; -.
DR   EMBL; AJ133483; CAC88120.1; JOINED.
DR   EMBL; AJ133484; CAC88120.1; JOINED.
DR   EMBL; AJ133485; CAC88120.1; JOINED.
SQ   SEQUENCE   1182 AA;  128585 MW;  715233D912C352F2 CRC64;

  Query Match           89.3%;  Score 5599;  DB 2;  Length 1182;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 1074;  Conservative   43;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              | |   | ||||||||||||::|| ||||||:|||||||||||||||||| ||:|||||||
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              |||:|||||||||:|:|||:|||||||||||||||||||||||||||||||||||||||
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||| |:|||||| ||||||||||||||||||||||||||||||||||||||||| |||||
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              |||||||||||||| ||| |||||||| ||||||||| ||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              | ||| ||:|||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              |||||||| |||||||||||||||||| |||||| ||||||||||||||||||||||||
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              |||:|||||||||||||||||||||||||||||||||||||||||||||:||||||||:
Db        421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              | | ||| |||||||: ||||| |||:||| || ||||||||||||||||||||||| |
Db        481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              |||||||||||||||| ||||||||||||||||||:|||||||  ||||||||||||
Db        541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              |||||||||||||||||||||: | |||||||:|||||||||| ||| |  :|||:
Db        601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              | || | |||||||||||||||: |||:||: |||||||||||||||||||||||||||||
Db        661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||:|||||||||||||||||||| ||||||||||||||||||||:||||||||||
Db        781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              |||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||
Db        901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              |||||:|||||||||||||||: |||||||| ||| |||||||||:||||||||||||:
Db       1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||:|||| |||||||||||:|||||||||||||:|:|:|:|||||: |: ||| ||
Db       1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
              |||    :||||||||||||:||||||||:||| :||
Db       1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181


RESULT 7
Q9DEF3
ID   Q9DEF3      PRELIMINARY;      PRT;  1413 AA.
AC   Q9DEF3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Patched-2.
GN   Name=Xptch-2;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20500895; PubMed=11044611;
RA   Takabatake T., Takahashi T.C., Takabatake Y., Yamada K., Ogawa M.,
RA   Takeshima K.;
RT   "Distinct expression of two types of Xenopus Patched genes during
RT   early embryogenesis and hindlimb development.";
RL   Mech. Dev. 98:99-104(2000).
DR   EMBL; AB037688; BAB18575.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
SQ   SEQUENCE   1413 AA;  157372 MW;  1215D2D7733E7F17 CRC64;

  Query Match           65.7%;  Score 4119;  DB 2;  Length 1413;
  Best Local Similarity   65.4%;  Pred. No. 1e-267;
  Matches  789;  Conservative  165;  Mismatches  213;  Indels   39;  Gaps    9;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |  ||  |     |||||||| || ||||||| ||||||||:||| |||
Db         35 PSYC-HAAFALKQIAKGKAVGQKAPLWLRAQFQALLFSLGCSIQRHCGKVLFIGLLVFGA 93
```

```
Qy        69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        94 LAVGLRVASIETDIERLWVEAGSRVSHELRYTKEKLGEESVYTSQMLIQTPKREGENILT 153

Qy       129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db       154 HEALLLHLRAALAASKVQVSMYGKSWDLNKICYKSGVPIIENGMIERMIEKLFPCVIITP 213

Qy       189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYV 248
Db       214 LDCFWEGSQLQGGSAYLPGRADIQWTNLDPIRLMEELGQFTSLDGFKEMLDKAEVGQAYM 273

Qy       249 GRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQG 308
Db       274 ERPCLDPTDSDCPESSPNKKTKKNPDIVSTLRGGCYGFSKKFMYWQKELILGGMLKGPNG 333

Qy       309 ELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALP 368
Db       334 ELKSAEALQTMYLLMSPGQLFEHFKDDYEIHDINWNEEKAAAILESWQRKFVEQAQQSVP 393

Qy       369 ENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLA 428
Db       394 QNSSQDIHAFSTTTLNDIMKSFSDVSAIRVAGGYLLMLAYACVTLLRWDCSKSQGAVGLA 453

Qy       429 GVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQ 488
Db       454 GVLLVALSVASGLGLCSLLGISFNAATTQVLPFLALGIGVDDMFLLAHAFTETSRSTPFK 513

Qy       489 ERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPA 548
Db       514 DRTGECLRRTGTSVTLTSINNMIAFFMAALVPIPALRAFSLQAAVIVVFNFAMVLLIFPA 573

Qy       549 ILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDG--------------TVPVGIA 594
Db       574 ILSLDLQRREDQRLDILCCFYSPCSSRVIQIQPQEFSDANDNHTYHPSSYGNPTITTS-T 632

Qy       595 HLTATVQAFTHCEASSQHVVTILPPQAHLVPPPS------DPLGSELFSPGGSTRDLLGQ 648
Db       633 QITTTVQAFTQCDPSGHHIVTILPPTSQISTSPSVIVPTMDPLGSQIFTPSSSTRDLLAQ 692

Qy       649 EEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQ 708
Db       693 LDESKEKRECVPLPFLKWSLSDFAREKYAPVLLKAETKGIVVTLFMALLGLGLYGTTMVH 752

Qy       709 DGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKA 768
Db       753 DGLYLTDIVPRETKEYNFISAQFKYFSFYNMFIVTKDGFDYPKAQESLYDLHEAFGSVKY 812

Qy       769 VLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTG 828
Db       813 VVREEGRDLPKMWLHYFQDWLRGLQTSFDMDWESGYITQDSYRNGTEDGVLAYKLLIQTG 872

Qy       829 DAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHD 888
Db       873 NKKEPFNFNQLTSRRLVDEKGLIPQDAFYIYLTVWVSNDPLGYAASQANFYPQPPEWIHD 932

Qy       889 KYDTTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSG 948
Db       933 RYDTTGENLRIPATEPIEFAQFPFYLNGLRQTSDFVEAIESVRSVCEEFVKQGVHSYPSG 992

Qy       949 SPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMG 1008
Db       993 YPFLFWEQYIGLRHWFLLAISIVLACTFLVCAILLLNPWTAGIIVFILAMMTVELFGIMG 1052

Qy      1009 FLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAIS 1068
Db      1053 LIGIKLSAIPVVILIASVGIGVEFTVHVALGFLTAIGDRNQRSVLALEHMFAPVLDGAIS 1112

Qy      1069 TLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI------Q 1122
Db      1113 TLLGVLMLAGSEFDFILRYFFAVLTILTILGLLNGLVLLPVLLSLIGPPAEVTPADNSSR 1172
```

```
Qy      1123 MYKESPEILSPPAPQGGGLRWGASSSLPQS----FARVTTSMTVAIHPPPL--PGAYIHP 1176
Db      1173 LPTPTPEPLPPPLSHHAFYMNHKGFSDPEDSSEYYSETTTTSGIEEDDPQLYERSAYI-- 1230

Qy      1177 APDEPP 1182
Db      1231 IPPKPP 1236
```

RESULT 8
Q6IRA5
ID Q6IRA5 PRELIMINARY; PRT; 1422 AA.
AC Q6IRA5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC070995; AAH70995.1; -.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
KW Hypothetical protein.
SQ SEQUENCE 1422 AA; 158128 MW; 2884B2656E60CE72 CRC64;

Query Match 65.5%; Score 4106; DB 2; Length 1422;
Best Local Similarity 65.3%; Pred. No. 7.9e-267;
Matches 787; Conservative 165; Mismatches 215; Indels 39; Gaps 9;

```
Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db          35 PSYC-HAAFALKQIAKGKAVGQKAPLWLRAQFQALLFILGCSIQRHCGKVLFIGLLVFGA 93

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db          94 LAVGLRVASIETDIERLWVEAGSRVSHELRYTKEKLGEESVYTSQMLIQTPKREGGNILT 153

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db         154 NEALLLHLRAALAASKVQVSMYGKSWDLNKICYKSGVPIIENGMIERMIEKLFPCVIITP 213

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYV 248
Db         214 LDCFWEGSQLQGGSAYLPGRADIQWTNLDPIKLMEELGQFTSLDGFKEMLDKAEVGQGYM 273

Qy         249 GRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQG 308
Db         274 ERPCLDPTDSDCPESSPNKKTKKKPDIVSTLRGGCYGFSKKFMYWQKELILGGMLKGPDG 333

Qy         309 ELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALP 368
Db         334 ELKSAEALQTMYLLMSPGQLYEHFKDDYEIHDINWNEEKAAAILESWQRKFVEQAQQSIP 393

Qy         369 ENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLA 428
Db         394 QNSSQDIHAFSTTTLNDIMKSFSDVSAIRVAGGYLLMLAYACATMLRWDCSKSQGAVGLA 453

Qy         429 GVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQ 488
Db         454 GVLLVALSVASGLGLCSLLGISFNAATTQVLPFLALGIGVDDMFLLAHAFTETSLSTPFK 513

Qy         489 ERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPA 548
Db         514 ERTGECLRRTGTSVALTSINNMIAFFMAALVPIPALRAFSLQAAVVVVFNFAMVLLIFPA 573

Qy         549 ILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDG--------------TVPVGIA 594
Db         574 ILSLDLHRREDQRLDILCCFYSPCSSRVIQIQPQEFSDANDNHTYHPSSYGNPTITTS-T 632

Qy         595 HLTATVQAFTHCEASSQHVVTILPPQAHLVPPPS------DPLGSELFSPGGSTRDLLGQ 648
Db         633 QITTTVQAFTQCDPSGHHIVTILPPTSQISTSPSVIVPTMDPLGSQVFSPSSSTRDLLAQ 692

Qy         649 EEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQ 708
Db         693 LDESKEKRECVPLPFLKWSLSDFAREKYAPVLLKAETKGIVVALFMALLGLGLYGTTMVH 752

Qy         709 DGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKA 768
Db         753 DGLYLTDIIPRETKEYNFISAQFKYFSFYNMFIVTKDGFNYPKAQESLYDLHEAFGSVRY 812

Qy         769 VLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTG 828
Db         813 VVREEGRDLPKMWLHYFQDWLRGLQTAFDKDWESGRMTQDNYRNGTEDGVLAYKLLIQTG 872

Qy         829 DAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHD 888
Db         873 NKKEPFNFNQLTSRRLVDEKGLIPQDAFYIYLTVWVSNDPLGYAASQANFYPQPPEWIHD 932

Qy         889 KYDTTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSG 948
Db         933 RYDTTGENLRIPAAEPIEFAQFPFYLNGLRQTSDFIEAIESVRSICEEFVKQGVHSYPSG 992

Qy         949 SPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMG 1008
Db         993 YPFLFWEQYIGLRHWFLLAISIVLACTFLVCAILLLNPWTAGIIVFILAMMTVELFGIMG 1052

Qy        1009 FLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAIS 1068
Db        1053 LIGIKLSAIPVVILIASVGIGVEFTVHVALGFLTAIGDRNQRSVLALEHMFAPVLDGAIS 1112

Qy        1069 TLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI------Q 1122
Db        1113 TLLGVLMLAGSEFDFILRYFFAVLTILTILGLLNGLVLLPVLLSLIGPPAEVTPADNGSR 1172

Qy        1123 MYKESPEILSPPAPQGGGLRWGASSSLPQS----FARVTTSMTVAIHPPPL--PGAYIHP 1176
Db        1173 LPTPTPEPLPPPLSHHAFYMNHKGFSDPEDSSEYYSETTTTSGLEEDDPRLYERSAYI-- 1230

Qy        1177 APDEPP 1182
Db        1231 IPPKPP 1236
```

RESULT 9
AAH70995
ID AAH70995 PRELIMINARY; PRT; 1422 AA.
AC AAH70995;
DT 24-MAY-2004 (TrEMBLrel. 27, Created)
DT 24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC070995; AAH70995.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1422 AA; 158128 MW; 2884B2656E60CE72 CRC64;

Query Match 65.5%; Score 4106; DB 2; Length 1422;
Best Local Similarity 65.3%; Pred. No. 7.9e-267;
Matches 787; Conservative 165; Mismatches 215; Indels 39; Gaps 9;

```
Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
```

```
Db        35 PSYC-HAAFALKQIAKGKAVGQKAPLWLRAQFQALLFILGCSIQRHCGKVLFIGLLVFGA 93

Qy        69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        94 LAVGLRVASIETDIERLWVEAGSRVSHELRYTKEKLGEESVYTSQMLIQTPKREGGNILT 153

Qy       129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db       154 NEALLLHLRAALAASKVQVSMYGKSWDLNKICYKSGVPIIENGMIERMIEKLFPCVIITP 213

Qy       189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYV 248
Db       214 LDCFWEGSQLQGGSAYLPGRADIQWTNLDPIKLMEELGQFTSLDGFKEMLDKAEVGQGYM 273

Qy       249 GRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQG 308
Db       274 ERPCLDPTDSDCPESSPNKKTKKKPDIVSTLRGGCYGFSKKFMYWQKELILGGMLKGPDG 333

Qy       309 ELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALP 368
Db       334 ELKSAEALQTMYLLMSPGQLYEHFKDDYEIHDINWNEEKAAAILESWQRKFVEQAQQSIP 393

Qy       369 ENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLA 428
Db       394 QNSSQDIHAFSTTTLNDIMKSFSDVSAIRVAGGYLLMLAYACATMLRWDCSKSQGAVGLA 453

Qy       429 GVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQ 488
Db       454 GVLLVALSVASGLGLCSLLGISFNAATTQVLPFLALGIGVDDMFLLAHAFTETSLSTPFK 513

Qy       489 ERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPA 548
Db       514 ERTGECLRRTGTSVALTSINNMIAFFMAALVPIPALRAFSLQAAVVVVFNFAMVLLIFPA 573

Qy       549 ILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDG--------------TVPVGIA 594
Db       574 ILSLDLHRREDQRLDILCCFYSPCSSRVIQIQPQEFSDANDNHTYHPSSYGNPTITTS-T 632

Qy       595 HLTATVQAFTHCEASSQHVVTILPPQAHLVPPPS------DPLGSELFSPGGSTRDLLGQ 648
Db       633 QITTTVQAFTQCDPSGHHIVTILPPTSQISTSPSVIVPTMDPLGSQVFSPSSSTRDLLAQ 692

Qy       649 EEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQ 708
Db       693 LDESKEKRECVPLPFLKWSLSDFAREKYAPVLLKAETKGIVVALFMALLGLGLYGTTMVH 752

Qy       709 DGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKA 768
Db       753 DGLYLTDIIPRETKEYNFISAQFKYFSFYNMFIVTKDGFNYPKAQESLYDLHEAFGSVRY 812

Qy       769 VLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTG 828
Db       813 VVREEGRDLPKMWLHYFQDWLRGLQTAFDKDWESGRMTQDNYRNGTEDGVLAYKLLIQTG 872

Qy       829 DAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHD 888
Db       873 NKKEPFNFNQLTSRRLVDEKGLIPQDAFYIYLTVWVSNDPLGYAASQANFYPQPPEWIHD 932

Qy       889 KYDTTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSG 948
Db       933 RYDTTGENLRIPAAEPIEFAQFPFYLNGLRQTSDFIEAIESVRSICEEFVKQGVHSYPSG 992

Qy       949 SPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMG 1008
Db       993 YPFLFWEQYIGLRHWFLLAISIVLACTFLVCAILLLNPWTAGIIVFILAMMTVELFGIMG 1052

Qy      1009 FLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAIS 1068
Db      1053 LIGIKLSAIPVVILIASVGIGVEFTVHVALGFLTAIGDRNQRSVLALEHMFAPVLDGAIS 1112

Qy      1069 TLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI------Q 1122
Db      1113 TLLGVLMLAGSEFDFILRYFFAVLTILTILGLLNGLVLLPVLLSLIGPPAEVTPADNGSR 1172

Qy      1123 MYKESPEILSPPAPQGGGLRWGASSSLPQS----FARVTTSMTVAIHPPPL--PGAYIHP 1176
Db      1173 LPTPTPEPLPPPLSHHAFYMNHKGFSDPEDSSEYYSETTTTSGLEEDDPRLYERSAYI-- 1230

Qy      1177 APDEPP 1182
Db      1231 IPPKPP 1236
```

RESULT 10
PTC1_BRARE
ID   PTC1_BRARE   STANDARD;   PRT; 1220 AA.
AC   Q98864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Patched protein homolog 1 (Patched 1) (PTC1).
GN   Name=ptc1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=96379744; PubMed=8787757;
RA   Concordet J.-P., Lewis K.E., Moore J.W., Goodrich L.V., Johnson R.L.,
RA   Scott M.P., Ingham P.W.;
RT   "Spatial regulation of the zebrafish patched homologue reflects the
RT   roles of sonic hedgehog and protein kinase A in neural tube and somite
RT   patterning.";
RL   Development 122:2835-2846(1996).
CC   -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC   hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC   smoothened protein (SMO) to transduce the hedgehog's proteins
CC   signal (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Detected in embryonic presomitic mesoderm,
CC   neuroectoderm, tissue surrounding the notochord, ventral neural
CC   tube.
CC   -!- DEVELOPMENTAL STAGE: At all stages, expression corresponds to the
CC   localization of SHH. First detected during gastrulation. By 36
CC   hours, PTC1 appears in the first branchial arch and the posterior
CC   mesenchyme of the fin bud; by 48 hours, in the hindbrain and
CC   foregut.
CC   -!- INDUCTION: Activated by Sonic hedgehog.
CC   -!- PTM: Glycosylation is necessary for SHH binding (By similarity).
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; X98883; CAA67386.1; -.
DR   PIR; T18291; T18291.
DR   ZFIN; ZDB-GENE-980526-44; ptc1.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Glycoprotein; Receptor; Transmembrane.
FT   DOMAIN   1   84   Cytoplasmic (Potential).
FT   TRANSMEM   85   105   Potential.

```
FT   DOMAIN      106    419       Extracellular (Potential).
FT   TRANSMEM    420    440       Potential.
FT   DOMAIN      441    449       Cytoplasmic (Potential).
FT   TRANSMEM    450    470       Potential.
FT   DOMAIN      471    484       Extracellular (Potential).
FT   TRANSMEM    485    505       Potential.
FT   DOMAIN      506    528       Cytoplasmic (Potential).
FT   TRANSMEM    529    549       Potential.
FT   DOMAIN      550    558       Extracellular (Potential).
FT   TRANSMEM    559    579       Potential.
FT   DOMAIN      580    739       Cytoplasmic (Potential).
FT   TRANSMEM    740    760       Potential.
FT   DOMAIN      761   1016       Extracellular (Potential).
FT   TRANSMEM   1017   1037       Potential.
FT   DOMAIN     1038   1044       Cytoplasmic (Potential).
FT   TRANSMEM   1045   1065       Potential.
FT   DOMAIN     1066   1072       Extracellular (Potential).
FT   TRANSMEM   1073   1093       Potential.
FT   DOMAIN     1094   1110       Cytoplasmic (Potential).
FT   TRANSMEM   1111   1131       Potential.
FT   DOMAIN     1132   1143       Extracellular (Potential).
FT   TRANSMEM   1144   1164       Potential.
FT   DOMAIN     1165   1220       Cytoplasmic (Potential).
FT   DOMAIN      421    579       SSD.
FT   DOMAIN      624    695       Thr-rich.
FT   CARBOHYD    397    397       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    865    865       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    888    888       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1220 AA;  135544 MW;  D10A9D04115F532D CRC64;
```

Query Match 64.5%; Score 4042.5; DB 1; Length 1220;
Best Local Similarity 64.6%; Pred. No. 1.2e-262;
Matches 775; Conservative 156; Mismatches 224; Indels 44; Gaps 8;

```
Qy          2 TRSPP------LRELPPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQ 52
              |||||      ||  |||   | | ||  |     |||||:|| ||  |||||| ||
Db         23 TRSPPPVNSDLLRR--PSYC-HAAFALKQISKGKAVGQKAPLWIRARFQAFLFSLGCHIQ 79

Qy         53 RHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTS 112
              |||||||||:||| ||||::|||:| |||::|:|||| |||||:|| ||||| |||: :||
Db         80 RHCGKVLFIGLLVFGALSVGLRVAAIETDIEKLWVEAGSRVSKELRYTKEKQGEESVFTS 139

Qy        113 QMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGM 172
              |||||| :||| |||| ||| |||:|||:|||||||||||||||||||:|||||:||| |
Db        140 QMLIQTPKQEGTNILTQEALLLHLEAALSASKVQVSLYGKSWDLNKICFKSGVPIIENVM 199

Qy        173 IEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLE 232
              || ||:|||||:|:|||||||||:|||||||||| ||||| |||| :|:||| | |||
Db        200 IERMIDKLFPCMIVTPLDCFWEGSKLQGGSAYLPGMPDIQWMNLDPLKLMEELSQFTSLE 259

Qy        233 GFRELLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMH 292
              ||||:|||||| ||: |||| | |  || ||||     | ||:| || ||||||| ||||
Db        260 GFREMLDKAQVGHAYMNRPCLDPSDTDCPHSAPNKDPWQVPNIAAELQGGCHGFSKKFMH 319

Qy        293 WQEELLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVL 352
              |||||:||    :| |   | |||||: ||||||:|||||: ||: ||| |:|::|: :|
Db        320 WQEELILGERVKDSQNALQSAEALQTMFLLMSPKQLYEHFKDDYEIHDINWNEDKATAIL 379

Qy        353 QAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVT 412
              ::|||:||::   ::|:|:|  ::|||:|||:||: :||:||  || ||||||||||||
Db        380 ESWQRKFVEVVHGSIPQNSSSNVYAFSTTTLNDIMKSFSDVSVIRVAGGYLLMLAYACVT 439

Qy        413 MLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVF 472
              |||||||:|||:|||||||||||:||:|||||:|||::|||||||||| |||||||||:|
Db        440 MLRWDCAKSQGAVGLAGVLLVALSVAAGLGLCSLLGLSFNAATTQVLPSLALGIGVDDMF 499

Qy        473 LLAHAFTEALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAA 532
              || |:|||     | :|| |:||:|||||| |||:||| || ||||||||||||||||
Db        500 LLGHSFTETRSNIPFKERTGDCLRRTGTSVALTSVNNMIAFFMAALVPIPALRAFSLQAA 559

Qy        533 IVVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------ 586
              :||   |  :|:|||||||| ||  :|||:|||| ||||::|||| |||| |
Db        560 VVVVFNFAMALLIFPAILSLDLHRREDKRLDILCCFYSPCSSRVIQIQPQELSDANDNHQ 619

Qy        587 ---------GTVPVGIAHLTATVQAFTHCEASSQHVVTILPPQAHL-VPPPS-------- 628
                      |:      |:| |||||| |:|: ||:|||||| : :   |||
Db        620 RAPATPTYTGSTITTSTHITTTVQAFTQCDAAGQHIVTILPPTSQISTTPPSMVLSTPTP 679

Qy        629 --DPLGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAK 686
                || ||::|:   |||||| | || ::    |  ||  ||||: ||| ::|||||:   |
Db        680 TTDPYGSQVFTTSSSTRDLLAQVEEPKEGRECVPLPFFRWNLSSFAREKYAPLLLKPETK 739

Qy        687 AIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGG 746
              :|:|:| ||| ||||| |:| ||| |||:||| |:|: |::|| :||| | : |||  |
Db        740 TVVVVVFVALLSLSLYGTTMVHDGLYLTDIVPRDTQEYEFITAQFKYFSFYNMYLVTMDG 799

Qy        747 FDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRIT 806
              |||| ||| |  ||  |:|:| |:     : || ||||:::||:|:|| || || :|:||
Db        800 FDYARSQRQLLQLHNAFNSVKYVVKDGNHKLPRMWLHYFQDWLKGLQATFDADWEAGKIT 859

Qy        807 RHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSS 866
              |||||:|||||||| |||||  :|| ::||||:|:||| :|||||:||: ||||||:
Db        860 YDSYRNGTEDGALAYKPLIQTGSKKEPFNYSQLTSRRLVDGDGLIPPEVFYIYLTVWVSN 919

Qy        867 DPLGLAASQANFYPPPPEWLHDKYDTTGENLRIPPAQPLEFAQFPPFLLRGLQKTADFVEA 926
              |||| |||||||||| | ||:|||||||||||||| |:|||||||| | ||:: :||:||
Db        920 DPLGYAASQANFYPHPREWIHDKYDTTGENLRIPAAEPLEFAQFPPFYLNGLRQASDFIEA 979

Qy        927 IEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNP 986
              ||  |  | |  : |:  ||:| |||||||:|||  |||:: ::| |||||||:|||||
Db        980 IESVRTICEEFMRQGIKNYPNGYPFLFWEQYIGLRHWFLLSISVVLACTFLVCAILLLNP 1039

Qy        987 WTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGS 1046
              ||||:|| :| |||||||||| :||||||||||||:|||||||||||:|||||| |
Db       1040 WTAGVIVFILPMMTVELFGIMGLIGIKLSAIPVVILIASVGIGVEFTVHIALGFLTAIGD 1099

Qy       1047 RNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVL 1106
              || |:| |:|| |||| |||||||||:|||||| ||||:||||| | :|||||:|:||||
Db       1100 RNTRSAVAMEHMFAPVIDGAISTLLGVLMLAGSEFDFIMRYFFAVLAILTLLGILNGLVL 1159

Qy       1107 LPVLLSILGPPPEVI------QMYKESPEILSPPAPQGGGLRWGASSSLPQSFARVTTS 1159
              ||||||:||| ||:       :  ||| : ||     |         :  |:|:  : |
Db       1160 LPVLLSLMGPPAEVVPANNANHLQSPSPEPMPPPMNHHGYYAGHIPKASHQAFSETSDS 1218
```

```
RESULT 11
PTC1_HUMAN
ID   PTC1_HUMAN     STANDARD;      PRT;  1447 AA.
AC   Q13635; Q13463;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Patched protein homolog 1 (PTC1) (PTC).
GN   Name=PTCH; Synonyms=PTCH1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANTS BCC PRO-175 AND PRO-ASN-ILE-815 INS.
RC   TISSUE=Lung;
RX   MEDLINE=96247324; PubMed=8658145;
RA   Johnson R.L., Rothman A.L., Xie J., Goodrich L.V., Bare J.W.,
RA   Bonifas J.M., Quinn A.G., Myers R.M., Cox D.R., Epstein E.H. Jr.,
RA   Scott M.P.;
RT   "Human homolog of patched, a candidate gene for the basal cell nevus
RT   syndrome.";
RL   Science 272:1668-1671(1996).
RN   [2]
RP   SEQUENCE OF 152-1447 FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=96218118; PubMed=8647801;
RA   Hahn H., Christiansen J., Wicking C., Zaphiropolous P.G.,
RA   Chidambaram A., Gerrard B., Vorechovsky I., Bale A.E., Toftgard R.,
RA   Dean M., Wainwright B.J.;
RT   "A mammalian patched homolog is expressed in target tissues of sonic
```

```
RT   hedgehog and maps to a region associated with developmental
RT   abnormalities.";
RL   J. Biol. Chem. 271:12125-12128(1996).
RN   [3]
RP   VARIANTS BCNS ARG-509; VAL-509; GLN-816 DEL AND TYR-1132.
RX   MEDLINE=96438609; PubMed=8840969;
RA   Chidambaram A., Goldstein A.M., Gailani M.R., Gerrard B., Bale S.J.,
RA   DiGiovanna J.J., Bale A.E., Dean M.;
RT   "Mutations in the human homologue of the Drosophila patched gene in
RT   Caucasian and African-American nevoid basal cell carcinoma syndrome
RT   patients.";
RL   Cancer Res. 56:4599-4601(1996).
RN   [4]
RP   VARIANTS BCNS TYR-513 AND ARG-1069.
RX   MEDLINE=97136566; PubMed=8981943;
RA   Wicking C., Shanley S., Smyth I., Gillies S., Negus K., Graham S.,
RA   Suthers G., Haites N., Edwards M., Wainwright B.J.,
RA   Chenevix-Trench G.;
RT   "Most germ-line mutations in the nevoid basal cell carcinoma syndrome
RT   lead to a premature termination of the PATCHED protein, and no
RT   genotype-phenotype correlations are evident.";
RL   Am. J. Hum. Genet. 60:21-26(1997).
RN   [5]
RP   VARIANT NBCCS ASP-1438.
RX   MEDLINE=98001068; PubMed=9341860;
RA   Lench N.J., Telford E.A.R., High A.S., Markham A.F., Wicking C.,
RA   Wainwright B.J.;
RT   "Characterisation of human patched germ line mutations in naevoid
RT   basal cell carcinoma syndrome.";
RL   Hum. Genet. 100:497-502(1997).
RN   [6]
RP   VARIANT PRO-1315.
RX   MEDLINE=99211211; PubMed=10200051;
RX   DOI=10.1002/(SICI)1098-1004(1998)11:6<480::AID-HUMU9>3.3.CO;2-W;
RA   Hasenpusch-Theil K., Bataille V., Laehdetie J., Obermayr F.,
RA   Sampson J.R., Frischauf A.-M.;
RT   "Gorlin syndrome: identification of 4 novel germ-line mutations of the
RT   human patched (PTCH) gene.";
RL   Hum. Mutat. 11:480-480(1998).
RN   [7]
RP   VARIANTS BCNS SER-376 AND VAL-1083 INS, AND VARIANT BCC TRP-1114.
RX   MEDLINE=98281604; PubMed=9620294;
RA   Aszterbaum M., Rothman A.L., Johnson R.L., Fisher M., Xie J.,
RA   Bonifas J.M., Zhang X., Scott M.P., Epstein E.H. Jr.;
RT   "Identification of mutations in the human PATCHED gene in sporadic
RT   basal cell carcinomas and in patients with the basal cell nevus
RT   syndrome.";
RL   J. Invest. Dermatol. 110:885-888(1998).
RN   [8]
RP   VARIANT PRO-1315.
RX   MEDLINE=20334946; PubMed=10874314;
RX   DOI=10.1002/1098-1004(200007)16:1<89::AID-HUMU18>3.3.CO;2-Z;
RA   Dong J., Gailani M.R., Pomeroy S.L., Reardon D., Bale A.E.;
RT   "Identification of PATCHED mutations in medulloblastomas by direct
RT   sequencing.";
RL   Hum. Mutat. 16:89-90(2000).
RN   [9]
RP   VARIANT BCNS PRO-1132.
RX   MEDLINE=21154106; PubMed=11231326;
RA   Reifenberger J., Arnold N., Kiechle M., Reifenberger G., Hauschild A.;
RT   "Coincident PTCH and BRCA1 germline mutations in a patient with nevoid
RT   basal cell carcinoma syndrome and familial breast cancer.";
RL   J. Invest. Dermatol. 116:472-474(2001).
RN   [10]
RP   VARIANTS SQUAMOUS CELL CARCINOMA MET-829 AND LYS-1242.
RX   MEDLINE=21184537; PubMed=11286632;
RA   Ping X.L., Ratner D., Zhang H., Wu X.L., Zhang M.J., Chen F.F.,
RA   Silvers D.N., Peacocke M., Tsou H.C.;
RT   "PTCH mutations in squamous cell carcinoma of the skin.";
RL   J. Invest. Dermatol. 116:614-616(2001).
CC   -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC       hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC       smoothened protein (SMO) to transduce the hedgehog's proteins
CC       signal. Seems to have a tumor suppressor function, as inactivation
CC       of this protein is probably a necessary, if not sufficient step
CC       for tumorigenesis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: In the adult, expressed in brain, lung, liver,
CC       heart, placenta, skeletal muscle, pancreas and kidney. Expressed
CC       in tumor cells but not in normal skin.
CC   -!- DEVELOPMENTAL STAGE: In the embryo, found in all major target
CC       tissues of sonic hedgehog, such as the ventral neural tube,
CC       somites, and tissues surrounding the zone of polarizing activity
CC       of the limb bud.
CC   -!- PTM: Glycosylation is necessary for SHH binding (By similarity).
CC   -!- DISEASE: Defects in PTCH are probably the cause of basal cell
CC       nevus syndrome (BCNS) [MIM:109400]; also known as Gorlin syndrome
CC       or Gorlin-Goltz syndrome. BCNS is an autosomal dominant disease
CC       characterized by nevoid basal cell carcinomas (NBCCS) and
CC       developmental abnormalities such as rib and craniofacial
CC       alterations, polydactyly, syndactyly, and spina bifida. In
CC       addition, the patients suffer from a multitude of tumors like
CC       basal cell carcinomas (BCC), fibromas of the ovaries and heart,
CC       cysts of the skin, jaws and mesentery, as well as medulloblastomas
CC       and meningiomas. PTCH is also mutated in squamous cell carcinoma
CC       (SCC). Could also be associated with large body size observed in
CC       BCNS patients.
CC   -!- DISEASE: Defects in PTCH are a cause of sporadic basal cell
CC       carcinoma (BCC) [MIM:605462].
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   -!- DATABASE: NAME=PTCH mutation database;
CC       WWW="http://www.cybergene.se/PTCH/ptchbase.html".
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PTCH100.html".
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U59464; AAC50550.1; -.
DR   EMBL; U43148; AAC50496.1; -.
DR   Genew; HGNC:9585; PTCH.
DR   MIM; 601309; -.
DR   MIM; 109400; -.
DR   MIM; 605462; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Anti-oncogene; Disease mutation; Glycoprotein; Polymorphism; Receptor;
KW   Transmembrane.
FT   DOMAIN       1    100       Cytoplasmic (Potential).
FT   TRANSMEM   101    121       Potential.
FT   DOMAIN     122    436       Extracellular (Potential).
FT   TRANSMEM   437    457       Potential.
FT   DOMAIN     458    472       Cytoplasmic (Potential).
FT   TRANSMEM   473    493       Potential.
FT   DOMAIN     494    501       Extracellular (Potential).
FT   TRANSMEM   502    522       Potential.
FT   DOMAIN     523    547       Cytoplasmic (Potential).
FT   TRANSMEM   548    568       Potential.
FT   DOMAIN     569    577       Extracellular (Potential).
FT   TRANSMEM   578    598       Potential.
FT   DOMAIN     599    748       Cytoplasmic (Potential).
```

```
FT   TRANSMEM     749     769       Potential.
FT   DOMAIN       770    1027       Extracellular (Potential).
FT   TRANSMEM    1028    1048       Potential.
FT   DOMAIN      1049    1055       Cytoplasmic (Potential).
FT   TRANSMEM    1056    1076       Potential.
FT   DOMAIN      1077    1083       Extracellular (Potential).
FT   TRANSMEM    1084    1104       Potential.
FT   DOMAIN      1105    1121       Cytoplasmic (Potential).
FT   TRANSMEM    1122    1141       Potential.
FT   DOMAIN      1142    1154       Extracellular (Potential).
FT   TRANSMEM    1155    1175       Potential.
FT   DOMAIN      1176    1447       Cytoplasmic (Potential).
FT   DOMAIN        14      31       Gly-rich.
FT   DOMAIN       438     598       SSD.
FT   CARBOHYD     141     141       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     312     312       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     349     349       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     414     414       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     875     875       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1000    1000       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT      175     175       L -> P (in BCNS; sporadic BCC).
FT                                  /FTId=VAR_007843.
FT   VARIANT      376     376       F -> S (in BCNS).
FT                                  /FTId=VAR_007844.
FT   VARIANT      509     509       G -> R (in BCNS; could be a rare
```

Query Match 53.4%; Score 3348; DB 1; Length 1447;
Best Local Similarity 49.9%; Pred. No. 7.4e-216;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

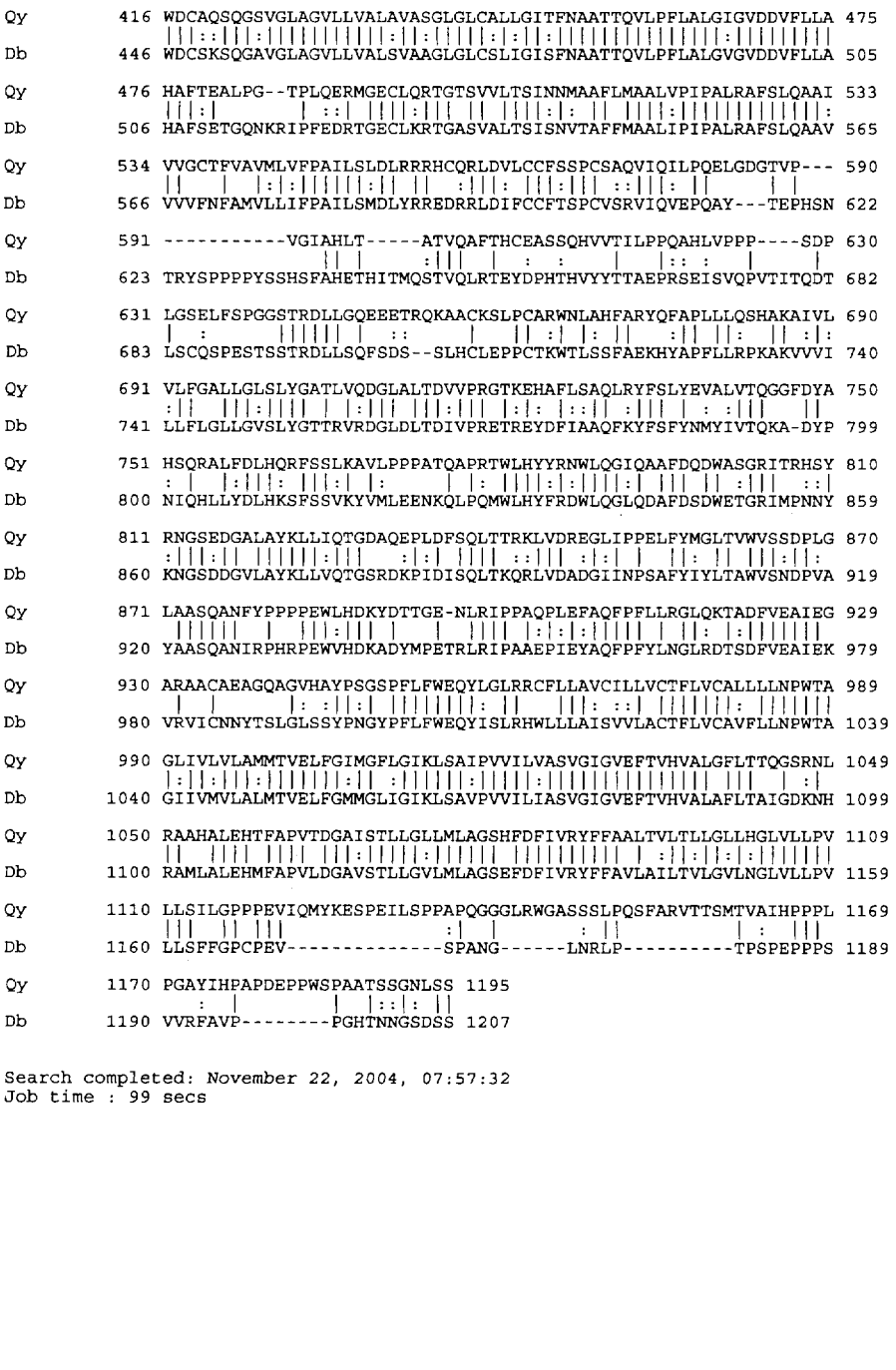
```
Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               ||:|| | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||| |:||| |:| ::||| || : ||||     :: : |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:| |  || :||| :| :  ::|  |:||||| | |:||||||::||  ::
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||| :||:||  ||  |||||||||:||||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
               |||||||||:||:|||||:|:||:||||||||||||||:||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   | |:|
Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||  |          |  :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   |:: :   |     | |  :      ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::     |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  |||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:|||||| | ||: |:|||||||  |  |:     |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :||||||:|||||:|||||||||||||||| |||  | :| ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139
                   ::  |||          ||                              | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140
               |
Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                 ||:|
Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
               :||     |:|||:||||:||   :|
Db        1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

```
RESULT 12
Q90XB9
ID   Q90XB9      PRELIMINARY;      PRT;   913 AA.
AC   Q90XB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Patched 2 (Fragment).
GN   Name=PTC2;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pearse R.V. Jr., Vogan K.J., Tabin C.J.;
RT   "Ptc1 and Ptc2 Transcripts Provide Distinct Readouts of Hedgehog
RT   Signaling Activity during Chick Embryogenesis.";
RL   Dev. Biol. 0:0-0(2001).
DR   EMBL; AF409095; AAK97655.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008158; F:hedgehog receptor activity; IEA.
```

```
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
FT   NON_TER     913     913
SQ   SEQUENCE   913 AA;  101047 MW;  DBD8117E5D842F33 CRC64;

  Query Match           53.3%;  Score 3344;  DB 2;  Length 913;
  Best Local Similarity   69.5%;  Pred. No. 7.5e-216;
  Matches  631;  Conservative  112;  Mismatches  139;  Indels   26;  Gaps    4;

Qy         17 PARTAAPQILAGSLK--------APLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              | |:| |:  | :|:        ||||||| || |||:||| ||||||||||:||| |||
Db          5 PPRSAPPRAAAAALRKALPEGRGAPLWLRARFQALLFALGCRIQRHCGKVLFVGLLLFGA 64

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
              ||:|||:| :||::| |||| |||||||| |||||||||: |||||||||: ::|||||||
Db         65 LAVGLRVASVETDIEHLWVEAGSRVSQELRYTKEKLGEESVYTSQMLIQTPKREGENILT 124

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
              ||| |||:||| ||||||||||||||||||||||||:|||||||| |||||||||||||
Db        125 QEALQLHLEAALAASKVQVSLYGKSWDLNKICYKSGVPIIENGMIERMIEKLFPCVILTP 184

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYV 248
              ||||||||||||||||||||||||:|||| ||:|||| | |||||:||||||:|||||:
Db        185 LDCFWEGAKLQGGSAYLPGRPDIQWSNLDPLQLMEELGQFTSLEGFKELLDKAEVGQAYM 244

Qy        249 GRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQG 308
              |||| | | ||| |||| |:|:|:|:: |||||||||| ||| |||||:|||  :| ||
Db        245 ERPCLDPRDPHCPSSAPNKQSQQSPDIPAELSGGCHGFSRKFMRWQEELILGGTTKDSQG 304

Qy        309 ELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFVQLAQEALP 368
              :|| |||||: |||||||||||||: ||: ||| ||||:|  :|:||||:||:|||:::|
Db        305 KLLSAEALQTMFLLMSPRQLYEHFKDDYEIHDISWSEEKAGAILEAWQRKFVELAQDSIP 364

Qy        369 ENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVGLA 428
              ||:| |||||:|||:||: :||:||| || |||||||||||||||||::|||:||||
Db        365 PNATQNIHAFSTTTLNDIMKSFSDVSAIRVAGGYLLMLAYACVTMLRWDCSKSQGAVGLA 424

Qy        429 GVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQ 488
              |||||||:||||||||:||||:||||||||||||||||||:|||||||||      | :
Db        425 GVLLVALSVASGLGLCSLLGISFNAATTQVLPFLALGIGVDDMFLLAHAFTETSQHIPFK 484

Qy        489 ERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPA 548
              || ||||:|||||| |||::|| || |||||||||||||||||:||    |  |: :|||
Db        485 ERTGECLRRTGTSVALTSVSNMIAFFMAALVPIPALRAFSLQAAVVVVFNFAMVLFIFPA 544

Qy        549 ILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------GTVPVG------IAHL 596
              |||||| ||  :|||:|||| ||||::|||| |||| |       ||| |       :
Db        545 ILSLDLYRREKRRLDILCCFYSPCSSRVIQIQPQELADANDNHASTVPYGHPGVATSTQI 604

Qy        597 TATVQAFTHCEASSQHVVTILPPQAH------LVPPPSDPLGSELFSPGGSTRDLLGQEE 650
              | |||||| |: |  |:||:||| :       :: ||:|||||::|:|  |||||| | :
Db        605 TTTVQAFTQCDPSGHHIVTVLPPTSQVCTSPAVLLPPADPLGSQVFTPSSSTRDLLAQLD 664

Qy        651 ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDG 710
              | :    |  ||  ||:|: ||| ::|||||:  | :|:||| |||||||| |:| ||
Db        665 EAKGGRECVPLPLCRWSLSDFAREKYAPLLLQTQTKVVVVVLFLALLGLSLYGTTMVHDG 724

Qy        711 LALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVL 770
              | |||:||| || |||:||| :||| | : :|||:||| |  :| ||  ||| ||::| |:
Db        725 LYLTDIVPRDTKAHAFISAQFKYFSFYNMFIVTKGGFHYPGAQAALLSLHQAFSTVKYVV 784

Qy        771 PPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDA 830
                    |: ||||:::||:|:|| ||:|| :|||| ||||||||||||||||||:
Db        785 REGNHDLPKMWLHYFQDWLRGLQATFDRDWQAGRITHDSYRNGSEDGALAYKLLIQTGNK 844

Qy        831 QEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKY 890
              :|| :|:|||||:|||  |:|||: ||: |||| |:|||| ||||||||||||||:|||
Db        845 KEPFNFNQLTTRRLVDENGIIPPDTFYICLTVWASNDPLGFAASQANFYPPPPEWIHDKY 904

Qy        891 DTTGENLR 898
              ||||||||
Db        905 DTTGENLR 912


RESULT 13
PTC1_CHICK
ID   PTC1_CHICK     STANDARD;      PRT;  1442 AA.
AC   Q90693;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Patched protein homolog 1 (PTC1) (PTC).
GN   Name=PTCH; Synonyms=PTC;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Limb bud;
RX   MEDLINE=96205046; PubMed=8620849;
RA   Marigo V., Scott M.P., Johnson R.L., Goodrich L.V., Tabin C.J.;
RT   "Conservation in hedgehog signaling: induction of a chicken patched
RT   homolog by Sonic hedgehog in the developing limb.";
RL   Development 122:1225-1233(1996).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=97064175; PubMed=8906794;
RA   Marigo V., Davey R.A., Zuo Y., Cunningham J.M., Tabin C.J.;
RT   "Biochemical evidence that patched is the Hedgehog receptor.";
RL   Nature 384:176-179(1996).
CC   -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC       hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC       smoothened protein (SMO) to transduce the hedgehog's proteins
CC       signal.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expression is seen in the embryonic neural
CC       tube, sclerotome, visceral mesoderm, and limb bud.
CC   -!- DEVELOPMENTAL STAGE: In stage 10 embryo, expression is seen in
CC       neural tube, and at lower levels in the notochord, epithelial
CC       somites, endoderm and splanchnic mesoderm. At stage 18, PTC is
CC       broadly expressed in the neural tube but excluded from the cells
CC       of the floor plate. At stage 32, expression occurs in the
CC       mesodermal cells of the gastrointestinal tract.
CC   -!- INDUCTION: Activated by hedgehog; repressed by itself (Probable).
CC   -!- PTM: Glycosylation is necessary for SHH binding.
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U40074; AAC59898.1; -.
DR   PIR; T18538; T18538.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Glycoprotein; Receptor; Transmembrane.
FT   DOMAIN        1    101       Cytoplasmic (Potential).
FT   TRANSMEM    102    122       Potential.
FT   DOMAIN      123    436       Extracellular (Potential).
FT   TRANSMEM    437    457       Potential.
FT   DOMAIN      458    472       Cytoplasmic (Potential).
```

```
FT   TRANSMEM     473    493       Potential.
FT   DOMAIN       494    501       Extracellular (Potential).
FT   TRANSMEM     502    522       Potential.
FT   DOMAIN       523    547       Cytoplasmic (Potential).
FT   TRANSMEM     548    568       Potential.
FT   DOMAIN       569    577       Extracellular (Potential).
FT   TRANSMEM     578    598       Potential.
FT   DOMAIN       599    747       Cytoplasmic (Potential).
FT   TRANSMEM     748    768       Potential.
FT   DOMAIN       769   1026       Extracellular (Potential).
FT   TRANSMEM    1027   1047       Potential.
FT   DOMAIN      1048   1053       Cytoplasmic (Potential).
FT   TRANSMEM    1054   1074       Potential.
FT   DOMAIN      1075   1082       Extracellular (Potential).
FT   TRANSMEM    1083   1101       Potential.
FT   DOMAIN      1102   1120       Cytoplasmic (Potential).
FT   TRANSMEM    1121   1141       Potential.
FT   DOMAIN      1142   1153       Extracellular (Potential).
FT   TRANSMEM    1154   1174       Potential.
FT   DOMAIN      1175   1442       Cytoplasmic (Potential).
FT   DOMAIN       438    598       SSD.
FT   CARBOHYD     141    141       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     312    312       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     349    349       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     414    414       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     827    827       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     874    874       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     999    999       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1442 AA;  160577 MW;  973E5F17FB8B6E43 CRC64;

  Query Match             53.3%;  Score 3340;  DB 1;  Length 1442;
  Best Local Similarity   54.3%;  Pred. No. 2.6e-215;
  Matches  663;  Conservative  204;  Mismatches  304;  Indels   50;  Gaps   17;

Qy         12 PSYTPPARTAAPQILAG---SLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |   ||  |     :|||||| || |||:||| ||::||| | :||| : |
Db         54 PSYC-DAAFALEQIAKGRATGRRAPLWLRAKFQRLLFNLGCYIQKNCGKFLVVGLL-YSA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||| | :|||:|:|||||| |||:||:||::|:|||| :  |::||| :::| |:||
Db        112 FAVGLRAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPQEDGTNVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db        172 TEALRQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITEAGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
              |||||||||| |:||| |:| :|| | || : ||||      :| : |:|:||:||  |
Db        232 LDCFWEGAKLQSGTAYLLGKPPLQWINFDPLEFLEELKKINYQVESWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:| |  || :||| :| :  :||  |||||:| | |:||||||::||  ::
Db        292 MDRPCLNPADPDCPITAPNKNSTKPLDVALVLSGGCYGLSRKYMHWQEELIIGGTVKNSS 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
              |:|: |:|||: | ||:|:|:|||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db        352 GKLVSAQALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRMYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
              : :|::|:: :|::|||||| :||:|| || ||||||||||:|||||||:|||:||
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCAKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
              |||||||||:||:|||||:|:||:|||||||||||||||:||||||||||||:|
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:||||||||||||:||   |  |:|
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD------GTVPVGIAH--- 595
              :||||||:|| ||  :|||: |||:|||  :|||| ||   :      : |   :|
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVTRVIQIEPQAYAENDNICYSSPPPYSSHSFA 650

Qy        596 ------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRDL 645
                    : :||| |  : :|   |   |:: :   |      | |  :      |||||
Db        651 HETQITMQSTVQLRTEYDPHTQAYYTTAEPRSEISVQPVTVTQDSLSCQSPESASSTRDL 710

Qy        646 LGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGAT 705
              | |  ::      |   || :| |: ||   :|| ||:  || :|: ||  |||||||| |
Db        711 LSQFSDS--SVHCLEPPCTKWTLSTFAEKHYAPFLLKPKAKVVVIFLFLGLLGLSLYGTT 768

Qy        706 LVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSS 765
               |:||| |||:||| |:|: |::|| :||| | : :|||    || : |  |::|: ||:
Db        769 RVRDGLDLTDIVPRDTREYDFIAAQFKYFSFYNMYIVTQKA-DYPNVQHLLYELHRSFSN 827

Qy        766 LKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLI 825
              :  ||      | |: ||||:|:||||:| ||| || :|:||  :|:|||:|  ||||||:
Db        828 VTYVLLEGDRQLPKMWLHYFRDWLQGLQDAFDSDWETGKITYSNYKNGSDDAVLAYKLLV 887

Qy        826 QTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEW 885
               |||:  :|:| |||| ::||| :|:| |   ||: || |||:||:  ||||||  |  |||
Db        888 QTGNRAKPIDISQLTKQRLVDADGIINPNAFYIYLTAWVSNDPVAYAASQANIRPHRPEW 947

Qy        886 LHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHA 944
              :||| |   |  |||| |:|:|:|||||  | ||::|:|||||||  || |     |: :
Db        948 VHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRETSDFVEAIEKVRAICNNYTSLGIAS 1007

Qy        945 YPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELF 1004
              ||:| ||||||||:|||   ||:: ::| |||||||| ||||||||:||:|||:||||||
Db       1008 YPNGYPFLFWEQYIGLRHWLLLSISVVLACTFLVCALFLLNPWTAGIIVVVLALMTVELF 1067

Qy       1005 GIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTD 1064
              |:|| :||||||:|||||:|||||||||||||:|| |||   | :| ||  |||| |||| |
Db       1068 GMMGLIGIKLSAVPVVILIASVGIGVEFTVHIALAFLTAIGDKNRRAVLALEHMFAPVLD 1127

Qy       1065 GAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI--- 1121
              ||:|||||:||||| |||||||||| | :||:||:|:||||||||||  || |||
Db       1128 GAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPAC 1187

Qy       1122 ---QMYKESPEILSPPA------PQGGGLRWGASSSLPQSFARVTTSMTVAIH---PPPL 1169
                 ::   |||   ||:      | |      ||    |     : ::  :|
Db       1188 GRNRLPTPSPE--PPPSIVRFALPPGHTNNGSDSSDSEYSSQTTVSGISEELHHYEATQS 1245

Qy       1170 PGAYIHPAPDEPPWSPAATSS 1190
              ||  :|    |   :|    |
Db       1246 PGIPVHQVVVEATENPVFARS 1266


RESULT 14
Q6UY90
ID   Q6UY90      PRELIMINARY;      PRT;  1434 AA.
AC   Q6UY90;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Patched.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F344;
RX   MEDLINE=22381811; PubMed=12469128;
RA   Lai K., Kaspar B.K., Gage F.H., Schaffer D.V.;
RT   "Sonic hedgehog regulates adult neural progenitor proliferation in
RT   vitro and in vivo.";
RL   Nat. Neurosci. 6:21-27(2003).
DR   EMBL; AY357891; AAQ67738.1; -.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR004766; Patchedtm_recept.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00918; 2A060602; 1.
DR   PROSITE; PS50156; SSD; 1.
```

```
SQ   SEQUENCE   1434 AA;  159257 MW;  7166D3C426BFA136 CRC64;

  Query Match             53.2%;  Score 3339.5;  DB 2;  Length 1434;
  Best Local Similarity   54.4%;  Pred. No. 2.7e-215;
  Matches  667;  Conservative  196;  Mismatches  284;  Indels   79;  Gaps   18;

Qy          3 RSPPLREL--PPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGK 57
              |: | |:    |||    |  |  ||  |      ||||||| || ||| ||| ||::|||
Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86

Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
               | :||| ||| |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||
Db         87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy        118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177
              | ::|| |:|| |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|
Db        147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy        178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236
              | |:||:|:|||||||||||||| |:||| |:| ::||| || : |||       :: : |
Db        207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy        237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296
              :|:||:||  |: ||||:| |  || :||| :| :  :||  |:||| | | |:||||||
Db        267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy        297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355
              |::||  ::  |:|: | |||: | ||:|:|:|||||| || :| | |:|::|: :|:||
Db        327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy        356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415
              || :|::  :::  |::|:: :|::|||||||| :||:||  ||  ||||||||||:||||
Db        386 QRTYVEVVHQSVAPNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445

Qy        416 WDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLA 475
              |||::|||:||||||||||:||:|||||:|:||:|||||||||||||||:|||||||||
Db        446 WDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLA 505

Qy        476 HAFTEALPG--TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAI 533
              |||:|       | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:
Db        506 HAFSETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAV 565

Qy        534 VVGCTFVAVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVP--- 590
              ||   |:|:|||||:|| ||  :|||: |||:||| ::|||: ||      | |
Db        566 VVVFNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAY---TEPHSN 622

Qy        591 -----------VGIAHLT-----ATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDP 630
                        || |     :||| |  :  :     |   |:: :    |      |
Db        623 TRYSPPPPYSSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTITQDT 682

Qy        631 LGSELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVL 690
              |  :      ||||||  |  ::      |   || :| |: ||   :|| ||:  || :|:
Db        683 LSCQSPESTSSTRDLLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLRPKAKVVVI 740

Qy        691 VLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA 750
              :||  |||:|||| | |:||| |||:|||  |:|: |::|| :||| | : :|||   ||
Db        741 LLFLGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYP 799

Qy        751 HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSY 810
              :  |:|||: |||:| |:     | |: ||||:|:||||:| ||| || :|||  ::|
Db        800 NIQHLLYDLHKSFSSVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNNY 859

Qy        811 RNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLG 870
              :|||:|| ||||||:|||   :|:| |||| ::||| :|:|  |  ||: || |||:||:
Db        860 KNGSDDGVLAYKLLVQTGSRDKPIDISQLTKQRLVDADGIIINPSAFYIYLTAWVSNDPVA 919

Qy        871 LAASQANFYPPPPEWLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEG 929
              ||||||  |  |||:||| |   |||| |:|:|:||||| | ||: |:|||||||||
Db        920 YAASQANIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEK 979

Qy        930 ARAACAEAGQAGVHAYPSGSPPLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTA 989
              |  |     |: :\|:| \|||||||: ||   |||: ::| |||||||: |||||||
Db        980 VRVICNNYTSLGLSSYPNGYPPLFWEQYISLRHWLLLAISVVLACTFLVCAVFLLNPWTA 1039

Qy        990 GLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNL 1049
              |:||:|||:|||||||:|| :||||||:|||||:|||||||||||||| |||  | :|
Db       1040 GIIVMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNH 1099

Qy       1050 RAAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPV 1109
              ||  |||| |||| |||:|||||:||||| |||||||||| | :||:||:|:|||||||
Db       1100 RAMLALEHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPV 1159

Qy       1110 LLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLPQSFARVTTSMTVAIHPPPL 1169
              |||  || |||                :|  |       :  ||          | :  |||
Db       1160 LLSFFGPCPEV--------------SPANG------LNRLP----------TPSPEPPPS 1189

Qy       1170 PGAYIHPAPDEPPWSPAATSSGNLSS 1195
                :  |         |  |::|: ||
Db       1190 VVRFAVP--------PGHTNNGSDSS 1207


RESULT 15
AAQ67738
ID   AAQ67738    PRELIMINARY;      PRT;  1434 AA.
AC   AAQ67738;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Patched.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F344;
RX   MEDLINE=22381811; PubMed=12469128;
RA   Lai K., Kaspar B.K., Gage F.H., Schaffer D.V.;
RT   "Sonic hedgehog regulates adult neural progenitor proliferation in
RT   vitro and in vivo.";
RL   Nat. Neurosci. 6:21-27(2003).
DR   EMBL; AY357891; AAQ67738.1; -.
SQ   SEQUENCE   1434 AA;  159257 MW;  7166D3C426BFA136 CRC64;

  Query Match             53.2%;  Score 3339.5;  DB 2;  Length 1434;
  Best Local Similarity   54.4%;  Pred. No. 2.7e-215;
  Matches  667;  Conservative  196;  Mismatches  284;  Indels   79;  Gaps   18;

Qy          3 RSPPLREL--PPSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGK 57
              |: | |:    |||    |  |  ||  |      ||||||| || ||| ||| ||::|||
Db         28 RAAPDRDYLHRPSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK 86

Qy         58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQ 117
               | :||| ||| |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||
Db         87 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQ 146

Qy        118 TARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMI 177
              | ::|| |:|| |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|
Db        147 TPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQII 206

Qy        178 EKLFPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRE 236
              | |:||:|:|||||||||||||| |:||| |:| ::||| || : |||       :: : |
Db        207 EYLYPCLIITPLDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEE 266

Qy        237 LLDKAQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEE 296
              :|:||:||  |: ||||:| |  || :||| :| :  :||  |:||| | | |:||||||
Db        267 MLNKAEVGHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEE 326

Qy        297 LLLGGMARDPQGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW 355
              |::||  ::  |:|: | |||: | ||:|:|:|||||| || :| | |:|::|: :|:||
Db        327 LIVGGTVKNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSH-INWNEDRAAAILEAW 385

Qy        356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLR 415
              || :|::  :::  |::|:: :|::|||||||| :||:||  ||  ||||||||||:||||
Db        386 QRTYVEVVHQSVAPNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLR 445
```



Search completed: November 22, 2004, 07:57:32
Job time : 99 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 22, 2004, 05:38:23 ; Search time 78 Seconds
(without alignments)
5532.710 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6272	100.0	1203	2	AAY43261	Aay43261 Human pat
2	6272	100.0	1203	5	AAE19829	Aae19829 Human pat
3	6272	100.0	1203	6	ABG74104	Abg74104 Human pat
4	6248	99.6	1203	2	AAY28444	Aay28444 Human ptc
5	6238	99.5	1203	3	AAY92703	Aay92703 Human pat
6	5911	94.2	1146	3	AAY92225	Aay92225 Human pat
7	5599	89.3	1182	5	AAE19831	Aae19831 Mouse pat
8	3348	53.4	1447	2	AAR75375	Aar75375 Human pat
9	3348	53.4	1447	2	AAW52200	Aaw52200 Human pat
10	3348	53.4	1447	2	AAW72969	Aaw72969 Human pat
11	3348	53.4	1447	4	AAB67163	Aab67163 Human pat
12	3348	53.4	1447	5	AAE19830	Aae19830 Human pat
13	3348	53.4	1447	5	ABJ10931	Abj10931 TRC8 rela
14	3348	53.4	1447	5	AAG79571	Aag79571 Human pat
15	3348	53.4	1447	7	ABU62275	Abu62275 Human pat
16	3348	53.4	1447	7	ADD46678	Add46678 Human Pro
17	3348	53.4	1447	7	ADE94224	Ade94224 Human ptc
18	3348	53.4	1447	7	ADH62731	Adh62731 Human pat
19	3348	53.4	1447	8	ADE48989	Ade48989 Human pat
20	3337	53.2	1434	2	AAW52199	Aaw52199 Mouse pat
21	3337	53.2	1434	2	AAW72968	Aaw72968 Mouse pat
22	3337	53.2	1434	4	AAB67159	Aab67159 Murine pa
23	3337	53.2	1434	5	AAG79572	Aag79572 Mouse pat
24	3337	53.2	1434	7	ABU62271	Abu62271 Mouse pat
25	3337	53.2	1434	7	ADE94215	Ade94215 Murine pt
26	3337	53.2	1434	7	ADH62722	Adh62722 Mouse pat
27	3337	53.2	1434	8	ADE48980	Ade48980 Mouse pat
28	3335	53.2	1434	2	AAR94380	Aar94380 Mouse pat
29	3048	48.6	1296	2	AAW47157	Aaw47157 Nevoid ba
30	2627	41.9	529	2	AAW82586	Aaw82586 Human Pat
31	2236	35.7	1311	2	AAW52197	Aaw52197 Precis co
32	2235	35.6	1311	2	AAW72971	Aaw72971 Precis co
33	2235	35.6	1311	4	AAB67156	Aab67156 Butterfly
34	2235	35.6	1311	5	AAG79573	Aag79573 Butterfly
35	2235	35.6	1311	7	ABU62149	Abu62149 Buckeye p
36	2235	35.6	1311	7	ADE94209	Ade94209 Peacock b
37	2235	35.6	1311	7	ADH62716	Adh62716 Butterfly
38	2235	35.6	1311	8	ADE48974	Ade48974 Butterfly
39	1992	31.8	1286	4	ABB59092	Abb59092 Drosophil
40	1992	31.8	1286	5	ABJ10929	Abj10929 TRC8 rela
41	1961.5	31.3	1299	2	AAR86304	Aar86304 Drosophil
42	1961.5	31.3	1299	4	AAE05389	Aae05389 Human pat
43	1961.5	31.3	1299	4	AAB85751	Aab85751 Hedgehog
44	1961.5	31.3	1299	4	AAB31232	Aab31232 A consens
45	1961.5	31.3	1299	5	ABB79150	Abb79150 Patched p

ALIGNMENTS

RESULT 1
AAY43261
ID AAY43261 standard; protein; 1203 AA.
XX
AC AAY43261;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human patched-2 protein sequence.
XX
KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
KW cell proliferation; cell differentiation; testicular cancer; gut disease;
KW degenerative disorder; nervous system disorder; Parkinson's disease;
KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9953058-A1.
XX
PD 21-OCT-1999.
XX
PF 02-APR-1999; 99WO-US007417.
XX
PR 15-APR-1998; 98US-00060939.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 1999-620428/53.
DR N-PSDB; AAZ31717.
XX
PT New isolated human patched-2 gene, used to develop products for treating,
PT e.g. cancer and Alzheimer's disease.
XX
PS Claim 14; Fig 1; 124pp; English.
XX
CC This sequence represents the human patched-2 (ptch-2) protein of the
CC invention. The patched-2 polypeptides are signalling molecules,
CC specifically for signalling and mediator molecules in the hedgehog (hh)
CC cascade which are involved in cell proliferation and differentiation.
CC They can be used for the treatment of disorders which are mediated at
CC least in part by Hh, especially Dhh, e.g. testicular cancer. They can
CC also be used for treating degenerative disorders of the nervous system,
CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou

```
CC   Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
CC   addiction. Patched-2 agonists can be used to treat gut diseases, bone
CC   diseases, skin diseases, diseases of the testis (including infertility),
CC   ulcers, lung diseases, diseases of the pancreas, diabetes, and
CC   osteoporosis. Antagonists or agonists of patched-2 may be used for
CC   treating disorders or creating a desirable physiological condition
CC   effected by blocking Hh signalling, especially Dhh signalling, e.g.
CC   contraception or infertility treatment. The products can also be used for
CC   detection, diagnosis, drug screening and production of transgenic animals
XX
SQ   Sequence 1203 AA;

  Query Match             100.0%;  Score 6272;  DB 2;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF  60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR  120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL  180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK  240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG  300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV  360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ  420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE  480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV  540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV  600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS  660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG  720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT  780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT  840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP  900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL  960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203


RESULT 2
AAE19829
ID   AAE19829 standard; protein; 1203 AA.
XX
AC   AAE19829;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human patched-2 (Ptch-2) protein.
XX
KW   Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW   cytostatic; testicular cancer; hedgehog protein signalling.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          57. .76
FT                   /label= TM1
FT                   /note= "Transmembrane domain"
FT   Domain          394. .414
FT                   /label= TM2
FT                   /note= "Transmembrane domain"
FT   Domain          427. .449
FT                   /label= TM3
FT                   /note= "Transmembrane domain"
FT   Domain          458. .477
FT                   /label= TM4
FT                   /note= "Transmembrane domain"
FT   Domain          502. .524
FT                   /label= TM5
FT                   /note= "Transmembrane domain"
FT   Domain          532. .553
FT                   /label= TM6
FT                   /note= "Transmembrane domain"
FT   Domain          687. .705
FT                   /label= TM7
FT                   /note= "Transmembrane domain"
FT   Domain          964. .984
FT                   /label= TM8
FT                   /note= "Transmembrane domain"
FT   Domain          988. .1010
FT                   /label= TM9
FT                   /note= "Transmembrane domain"
FT   Domain          1014. .1033
FT                   /label= TM10
```

```
FT                   /note= "Transmembrane domain"
FT   Domain          1058. .1077
FT                   /label= TM11
FT                   /note= "Transmembrane domain"
FT   Domain          1091. .1114
FT                   /label= TM12
FT                   /note= "Transmembrane domain"
XX
PN   US6348575-B1.
XX
PD   19-FEB-2002.
XX
PF   15-APR-1999;   99US-00293505.
XX
PR   15-APR-1998;   98US-0081884P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage F,  Carpenter DA;
XX
DR   WPI; 2002-215260/27.
DR   N-PSDB; AAD31576.
XX
PT   Native human patched-2 polypeptide for treating disorders caused by
PT   Hedgehog protein signaling such as testicular cancer, and for screening
PT   cDNA libraries.
XX
PS   Example 1; Fig 1; 82pp; English.
XX
CC   The invention relates to an isolated sequence comprising a native human
CC   patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC   and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC   cell proliferation and differentiation. The isolated sequence is useful
CC   for the treatment of disorders which are linked to Hedgehog, especially
CC   Desert hedgehog expression, such as testicular cancer. It may also be
CC   used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC   homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC   Hedgehog protein signalling. The present sequence is human patched-2
CC   (Ptch-2) protein
XX
SQ   Sequence 1203 AA;

  Query Match             100.0%;  Score 6272;  DB 5;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203


RESULT 3
ABG74104
ID   ABG74104 standard; protein; 1203 AA.
XX
AC   ABG74104;
XX
DT   02-APR-2003  (first entry)
XX
DE   Human patched-2 protein.
XX
KW   Human; patched-2; Dhh signalling; proliferation; differentiation;
KW   chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW   basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW   Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease;
KW   Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
```

KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX
OS Homo sapiens.
XX
PN US2002156245-A1.
XX
PD 24-OCT-2002.
XX
PF 20-NOV-2001; 2001US-00990046.
XX
PR 15-APR-1998; 98US-0081884P.
PR 15-APR-1999; 99US-00293505.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage FJ, Carpenter DA;
XX
DR WPI; 2003-182650/18.
DR N-PSDB; ABX15919.
XX
PT New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT e.g., testicular cancer.
XX
PS Claim 14; Fig 1; 85pp; English.
XX
CC The invention relates to a new isolated nucleic acid encoding a
CC polypeptide having patched-2 biological activity, comprises DNA having at
CC least 95% sequence identity with a DNA molecule or its complement
CC encoding: (a) a human patched-2 polypeptide comprising the sequence
CC ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC Deposit No. 209778 designation). Also included are a vector comprising
CC the nucleic acid, a host cell transformed with the vector, a process for
CC producing patched-2 polypeptides, an isolated native sequence of human
CC patched-2 polypeptide, a chimaeric molecule comprising the vertebrate
CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC patched-2 that stimulates or enhances the normal functioning of patched-2
CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC and diagnosing to determine whether a particular disorder is modulated
CC The nucleic acid is useful for manufacturing a medicament for diagnosing
CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC Patched-2 may also be used to develop male contraceptives. The gene for
CC Patched-2 is located on human chromosome 1p33-34. The present sequence
CC represents human patched-2 protein
XX
SQ Sequence 1203 AA;

Query Match 100.0%; Score 6272; DB 6; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

RESULT 4
AAY28444

ID AAY28444 standard; protein; 1203 AA.
XX
AC AAY28444;
XX
DT 03-DEC-1999 (first entry)
XX
DE Human ptc-2 protein.
XX
KW Patched-2; ptc-2; human; hedgehog receptor; nootropic; neuroprotective;
KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
KW graft; transplant; treatment; nervous system injury; chemical injury;
KW vasal injury; infection; inflammatory; tumor-induced injury; ageing;
KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
KW Parkinson's disease; Huntingdon's chorea; amylotrophic lateral sclerosis;
KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
KW lesion-induced death; neuron regeneration; damage repair; skeletal;
KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
XX
OS Homo sapiens.
XX
PN WO9929854-A1.
XX
PD 17-JUN-1999.
XX
PF 08-DEC-1998; 98WO-US026009.
XX
PR 08-DEC-1997; 97US-0067940P.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Bumcrot DA;
XX
DR WPI; 1999-561298/47.
DR N-PSDB; AAX89478.
XX
PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
PT prevention and/or reduction of the severity of neurological conditions.
XX
PS Claim 3; Page 73-77; 80pp; English.
XX
CC This invention describes a novel recombinantly produced human patched-2
CC (ptc-2) polypeptide which has nootropic, neuroprotective, cardiant,
CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
CC protein is a hedgehog receptor and is therefore capable of modulating
CC hedgehog signalling, and so affect a number of hedgehog-mediated
CC biological activities. The human patched-2 (ptc-2) protein can be used to
CC screen for modulators, antagonists and agonists, which are likely to play
CC an important role in the modulation of cellular proliferation and
CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
CC tissues during disease states. Modulators of ptc-2 protein can be used
CC for in vivo reformation of tissue; to improve grafting and morphology of
CC transplanted tissue; for the treatment, prevention and/or reduction of
CC the severity of neurological conditions deriving from: injury to the
CC nervous system including traumatic injury, chemical injury, vasal injury
CC and deficits (such as ischemia resulting from stroke), together with
CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
CC system including Alzheimer's disease; chronic neurodegenerative diseases
CC of the nervous system including Parkinson's disease, Huntingdon's chorea,
CC amylotrophic lateral sclerosis, as well as spinocerebellar degenerations;
CC and chronic immunological diseases of the nervous system including
CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
CC of autonomic disorders of the peripheral nervous system, including
CC disorders affecting the innervation of smooth muscle and endocrine
CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
CC Antagonists of ptc-2 protein can be used to prevent differentiation of
CC cells in culture, as well as for treatment of chronic pain syndromes.
CC Agonists may be used to rescue neurons from lesion-induced death as well
CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)
CC infection, metabolic disease, nutritional deficiency, toxic agents, and
CC so on. ptc-2 therapeutics may also be used for the repair of central and
CC peripheral nerve damage, for repair and regeneration of non-neuronal
CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
CC for generation of prosthetic cartilage devices, and to induce
CC spermatogenesis and as fertility enhancers. This sequence represents the
CC human ptc-2 protein described in the invention
XX
SQ Sequence 1203 AA;

Query Match 99.6%; Score 6248; DB 2; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy   61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy  121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy  181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy  241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy  301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy  361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy  421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy  481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy  541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AVMLVFPAIFSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy  601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy  661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy  721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy  781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840

Qy  841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWMAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200

Qy       1201 ATG 1203

Db       1201 ATG 1203
```

RESULT 5
AAY92703
ID AAY92703 standard; protein; 1203 AA.
XX
AC AAY92703;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human patched 2 (PTCH2) protein splice variant.
XX
KW Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMM1;
KW familial adenomatous polyposis; hMom1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
XX
OS Homo sapiens.
XX
PN WO200020037-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-SE001784.
XX
PR 06-OCT-1998; 98SE-00003393.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
PI Hollingsworth RE;
XX
DR WPI; 2000-303645/26.
DR N-PSDB; AAA09084.
XX
PT Isolated human protein capable of participating in human patched
PT gene/Sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX
PS Disclosure; Page; 55pp; English.
XX
CC This protein is a splice variant encoded by the novel human patched 2
CC gene (PTCH2), which has been localised by radiation hybrid mapping to
CC chromosome 1p32-35 with D1S211 and WI1404 as closest flanking markers and
CC with an estimated localisation 5.5 cR from D1S443. This region is often
CC lost by LOH in various different tumour types, such as neuroblastoma,
CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour
CC suppressor gene in this region. It is also a candidate gene for
CC involvement in familial melanoma CMM1, modifier locus for familial
CC adenomatous polyposis hMom1 and Michelin Tire Baby Syndrome. PTCH2 is
CC capable of participating in the human patched gene/Sonic hedgehog
CC (PTCH/SHH) pathway during embryonic development and/or carcinogenesis.
CC The isolated human protein is useful as a medicament for the treatment of
CC a condition involving tumours such as BCC (basal cell carcinoma). The
CC nucleic acid is useful in gene therapy, and for use as a probe, primer or
CC a diagnostic agent. Note: This sequence was constructed using information
CC from Figure 2B and the protein sequence given on pages 41-44 of the
CC specification
XX
SQ Sequence 1203 AA;

```
  Query Match             99.5%;  Score 6238;  DB 3;  Length 1203;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1199;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180

Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
```

```
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQELLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENFRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGQLSSRGPGP 1200

Qy       1201 ATG 1203
              |||
Db       1201 ATG 1203
```

RESULT 6
AAY92225
ID AAY92225 standard; protein; 1146 AA.
XX
AC AAY92225;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human patched 2 (PTCH2) protein.
XX
KW Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
KW familial adenomatous polyposis; hMom1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW basal cell carcinoma; chromosome 1p32-35; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200020037-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-SE001784.
XX
PR 06-OCT-1998; 98SE-00003393.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
PI Hollingsworth RE;
XX
DR WPI; 2000-303645/26.
DR N-PSDB; AAA09081, AAA09084.
XX
PT Isolated human protein capable of participating in human patched
PT gene/Sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX
PS Claim 2; Page 41-44; 55pp; English.
XX
CC This protein is encoded by the novel human patched 2 gene (PTCH2), which
CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
CC D1S211 and WI1404 as closest flanking markers and with an estimated
CC localisation 5.5 cR from D1S443. This region is often lost by LOH in
CC various different tumour types, such as neuroblastoma, melanoma and
CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
CC gene in this region. It is also a candidate gene for involvement in
CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
CC hMom1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
CC exist (see AAA09082-84). PTCH2 is capable of participating in the human
CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
CC development and/or carcinogenesis. The isolated human protein is useful
CC as a medicament for the treatment of a condition involving tumours such
CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
CC therapy, and for use as a probe, primer or a diagnostic agent
XX
SQ Sequence 1146 AA;

Query Match 94.2%; Score 5911; DB 3; Length 1146;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1139; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
```

```
Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQELLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENFRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
Db        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
Db       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
Db       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140

Qy       1141 LR 1142
Db       1141 LR 1142
```

```
RESULT 7
AAE19831
ID   AAE19831 standard; protein; 1182 AA.
XX
AC   AAE19831;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Mouse patched-2 (Ptch-2) protein.
XX
KW   Mouse; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW   cytostatic; testicular cancer; hedgehog protein signalling.
XX
OS   Mus musculus.
XX
PN   US6348575-B1.
XX
PD   19-FEB-2002.
XX
PF   15-APR-1999;   99US-00293505.
XX
PR   15-APR-1998;   98US-0081884P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage F,  Carpenter DA;
XX
DR   WPI; 2002-215260/27.
XX
PT   Native human patched-2 polypeptide for treating disorders caused by
PT   Hedgehog protein signaling such as testicular cancer, and for screening
PT   cDNA libraries.
XX
PS   Example 1; Fig 8; 82pp; English.
XX
CC   The invention relates to an isolated sequence comprising a native human
CC   patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC   and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC   cell proliferation and differentiation. The isolated sequence is useful
CC   for the treatment of disorders which are linked to Hedgehog, especially
CC   Desert hedgehog expression, such as testicular cancer. It may also be
CC   used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC   homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC   Hedgehog protein signalling. The present sequence is mouse patched-2
```

```
CC   (Ptch-2) protein
XX
SQ   Sequence 1182 AA;

  Query Match             89.3%;  Score 5599;  DB 5;  Length 1182;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 1074;  Conservative   43;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVLF 60
Db          1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCRIQKHCGKVLF 60

Qy         61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAR 120
Db         61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTAH 120

Qy        121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
Db        121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIERMIEKL 180

Qy        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDK 240
Db        181 FPCVILTPLDCFWEGAKLQGGSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDK 240

Qy        241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG 300
Db        241 AQVGQAYVGRPCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG 300

Qy        301 GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db        301 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASMVLQAWQRRFV 360

Qy        361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
Db        361 QLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420

Qy        421 SQGSVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
Db        421 SQGAVGLAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDIFLLAHAFTK 480

Qy        481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
Db        481 APPDTPLPERMGECLRSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA 540

Qy        541 AVMLVFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV 600
Db        541 AVMLVFPAILSLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV 600

Qy        601 QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEEETRQKAACKS 660
Db        601 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEEGTGPQAACRP 660

Qy        661 LPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db        661 LLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLSLYGATLVQDGLALTDVVPRG 720

Qy        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
Db        721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780

Qy        781 WLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db        781 WLHYYRSWLQGIQAAFDQDWASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLT 840

Qy        841 TRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900
Db        841 TRKLVDKEGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP 900

Qy        901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db        901 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSPFLFWEQYLGL 960

Qy        961 RRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020
```

```
                |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        961 RRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVV 1020

Qy       1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSH 1080
                |||||:|||||||||||||||: |||||||| ||| |||||||||:||||||||||||:
Db       1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLLMLAGSN 1080

Qy       1081 FDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGG 1140
                ||||:|||| |||||||||||||:|||||||||||||:|:|:|||||: |:  ||| ||
Db       1081 FDFIIRYFFVVLTVLTLLGLLHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGG 1140

Qy       1141 LRWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPAPDEP 1181
                |||    :|||||||||||||||:||||||||:||| :||
Db       1141 LRWDRPPTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEP 1181


RESULT 8
AAR75375
ID   AAR75375 standard; protein; 1447 AA.
XX
AC   AAR75375;
XX
DT   30-JUL-1996  (first entry)
XX
DE   Human patched protein.
XX
KW   Patched gene; PTC protein; embryo development; cellular regulation;
KW   signal transduction; ligand; antibody; hedgehog protein.
XX
OS   Homo sapiens.
XX
PN   WO9611260-A1.
XX
PD   18-APR-1996.
XX
PF   06-OCT-1995;   95WO-US013233.
XX
PR   07-OCT-1994;   94US-00319745.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Scott MP,  Goodrich LV,  Johnson RL;
XX
DR   WPI; 1996-209842/21.
DR   N-PSDB; AAT14220.
XX
PT   DNA encoding patched protein other than Drosophila patched protein - used
PT   to produce antibodies which detect or inhibit patched protein ligand
PT   signal transduction in cells.
XX
PS   Example; Page 56-61; 70pp; English.
XX
CC   Human patched protein (PTC) (AAR75375) was identified as the product of a
CC   cDNA clone (AAT14220) derived from human lung. It has 96% identity and
CC   98% similarity to mouse PTC. PTC protein has been proposed as a receptor
CC   for hedgehog protein on the basis of genetic experiments in flies. Human
CC   PTC protein can be obtd. in large amounts by expression of the cDNA clone
CC   in transformed host cells. It can be used to screen for agonists and
CC   antagonists, to isolate its ligand, partic. Sonic hedgehog, to assay for
CC   the transcription of ptc mRNA and to raise antibodies
XX
SQ   Sequence 1447 AA;

  Query Match             53.4%;  Score 3348;  DB 2;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.5e-291;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||

Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
                 |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||| |:||| |:| ::||| || : ||||      :: : |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:| |  || :||| :| :  ::|  |:|||| | |:|||||::||  ::
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||||| :||:||  ||  ||||||||||:|||||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
               |||||||||:||:|||||:|:||:|||||||||||||||:||||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   |  |:|
Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |  :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   |:: :   |      | |  :      ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::     |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |  |:     |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| |||||||||:|||    || : ::| |||||||: |||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :||||||:|||||:|||||||||||||||| |||  | :| ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139
                   ::   |||         ||                              | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247
```

```
Qy       1140 G------------------------------------------------------------ 1140
              |
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                ||:|
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
              :||     |:|||:||||:||   :|
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 9
AAW52200
ID AAW52200 standard; protein; 1447 AA.
XX
AC AAW52200;
XX
DT 25-JUN-1998 (first entry)
XX
DE Human patched (ptc) protein.
XX
KW Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
KW wound healing; ageing; human.
XX
OS Homo sapiens.
XX
PN WO9745541-A2.
XX
PD 04-DEC-1997.
XX
PF 02-JUN-1997; 97WO-US009553.
XX
PR 31-MAY-1996; 96US-00656055.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (REGC) UNIV CALIFORNIA.
XX
PI Scott MP, Goodrich LV, Johnson RL, Epstein E, Oro A;
XX
DR WPI; 1998-032648/03.
DR N-PSDB; AAV21590.
XX
PT Patched protein other than Drosophila melanogaster patched protein - used
PT for characterising the phenotype of a tumour.
XX
PS Claim 4; Page 76-80; 86pp; English.
XX
CC This is a human patched (ptc) protein. The encoding DNA can be used to
CC construct an expression cassette comprising an altered patch or hedgehog
CC gene. The expression cassette comprises a nucleic acid encoding a patched
CC protein other than a Drosophila melanogaster patched protein, or fragment
CC of at least 12 nucleotides in length, as other than an intact chromosome
CC under transcriptional control of a transcriptional initiation region, and
CC a transcriptional termination region, both functional in an expression
CC host. A genetically engineered mammalian cell comprising this expression
CC cassette as an extrachromosomal element or integrated into the genome of
CC the cell can be predisposed to develop basal cell carcinoma as a result
CC of the transfection. By analysing DNA, functional analysis of patched
CC protein function, or by detecting antibody binding to abnormal patched
CC protein, a genetic predisposition to developmental abnormalities and
CC cancer can be diagnosed. This analysis can also be used for
CC characterising the phenotype of a tumour, particularly a carcinoma,
CC especially a basal cell carcinoma. The methods can also be used for
CC characterising transitional cell carcinoma of the bladder, meningiomas
CC medulloblastomas, etc. The modified cells comprising the expression
CC cassette can be used to determine the role of different exons of the
CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal
CC models created from these cells can be used as animal models for
CC carcinomas of the skin. The patched protein of mosquito, butterfly or
CC beetle or alternatively, a mammalian patched protein of human or mouse
CC can be used to identify ligands or substrates that bind to, modulate, or
CC mimic the action of patched gene. These agents could be used as tumour
CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing)
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 2; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
              |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
              |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
              |||||||||| |:||| |:| ::||| || : ||||      :: : |:|:||:||  |
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
              : ||||:| |  || :||| :| :  ::|  |:|||| | |:|||||||::||  ::
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
              |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
              : :|::|:: :|::|||||| :||:||  ||  |||||||||:|||||||::|||:||
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
              |||||||||:||:|||||:|:||:|||||||||||||||:||||||||||||:|
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
              | ::| ||||:||| || ||||:|: || |||||||||||||||:||    |  |:|
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
              :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |   :|
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |  |:: :  |     | |  :       ||||
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
              || |  ::     |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
              | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
              ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
              :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
              |:||| |   |  |||| |:|:|:|||||  | ||: |:|||||||  |  |:    |:
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007
```

```
Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
              :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
              ||:|| :||||||:|||||:|||||||||||||||| |||  | :| ||  |||| ||||
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
              |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139
                  ::   |||         ||                             | ||
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
              |
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                            |||                ||:|
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
              :||     |:|||:||||:||   :|
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 10
AAW72969
ID AAW72969 standard; protein; 1447 AA.
XX
AC AAW72969;
XX
DT 26-JAN-1999 (first entry)
XX
DE Human patched protein.
XX
KW Human; patched gene; diagnosis; treatment; developmental disorder;
KW cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
KW sperm production; gene therapy.
XX
OS Homo sapiens.
XX
PN US5837538-A.
XX
PD 17-NOV-1998.
XX
PF 06-OCT-1995; 95US-00540406.
XX
PR 07-OCT-1994; 94US-00319745.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
DR WPI; 1999-023461/02.
DR N-PSDB; AAV64093.
XX
PT Nucleic acid encoding vertebrate patched protein and related
PT transformants - used to express poly:peptide(s), useful for diagnosis and
PT treatment of developmental disorders or cancer, and in healing of injured
PT tissue.
XX
PS Claim 23; Col 63-70; 38pp; English.
XX
CC The present sequence represents the human patched (ptc) protein. Cells
CC containing and expressing the ptc gene are used for the recombinant
CC production of the protein. These in turn are useful: (i) for generating
CC antibodies (Ab); and (ii) to screen for specific-binding ligands
CC (potential therapeutic agonists and antagonists). The ptc gene, or its
CC fragments, are used to isolate related sequences from other mammals; to
CC identify mutations (particularly those associated with genetic diseases
CC such as spina bifida and other developmental disorders); to monitor
CC expression levels in testis (to determine relationship with sperm
CC production) and to isolate 5'-non-coding sequences (used to study
CC embryonic development and to provide regulated expression of proteins).
CC The complete gene can be used in gene therapy, including expression of
CC antisense molecules, and to generate transgenic animals for studies of
CC embryonic development. Ab are used diagnostically to determine the ptc
CC protein on cell surfaces and as competitive inhibitors of signal
CC transduction through the ptc ligand. Cells that have been engineered to
CC express the ptc protein can be used to promote regrowth and healing of
CC damaged tissue (e.g. growth of new teeth) and regulation of the ptc
CC protein expression may be useful in cancer treatment (it may control the
CC Wnt-1 oncogene)
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 2; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
              |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
              |||  || :|| ||:|  | :|  :  | |  :|||||  : | |  :: :|| |:||:|:||
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
              |||||||||| |:||| |:|  ::||| || : ||||      :: : |:|:||:||  |
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
              : ||||:| |  || :||| :| :  ::|  |:|||| | |:|||||||::||  ::
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
              |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
              : :|::|:: :|::|||||||| :||:||  ||  ||||||||||:|||||::|||:||
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
              |||||||||:||:|||||:|:||:|||||||||||||||:|||||||||||||:|
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
              | ::| ||||:||| || ||||:|: || ||||:|||||||||||||:||   |  |:|
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
              :||||||:|| ||  :|||: |||:||| ::|||: ||   |           |   :|
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :    |   |:: :   |      | |  :       ||||
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
              || |  ::    |   || :| |: ||   :|| ||:  || :|: ||  |||:||||
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
              | |:||| |||:||| |:|:  |::|| :||| | : :|||   || : |  |:|||: ||
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827
```

```
Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-------------------------------APQGG 1139
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 -----------------------------LRWG----------------ASSSLPQSFAR 1155
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 11
AAB67163
ID AAB67163 standard; protein; 1447 AA.
XX
AC AAB67163;
XX
DT 12-APR-2001 (first entry)
XX
DE Human patched protein.
XX
KW Human; patched; PTC; segment polarity; limb patterning; development;
KW hedgehog; antibody; mouse.
XX
OS Homo sapiens.
XX
PN US6172200-B1.
XX
PD 09-JAN-2001.
XX
PF 20-OCT-1997; 97US-00954668.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
XX
PA (STRD) UNIV LELAND S STANFORD.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
DR WPI; 2001-136884/14.
DR N-PSDB; AAF32185.
XX

PT Novel monoclonal antibody useful in diagnostic assays for detection of
PT presence of protein on surface of cells specifically binds to naturally
PT occurring patched protein, other than Drosophila patched protein.
XX
PS Disclosure; Col 61-70; 39pp; English.
XX
CC The present invention provides a monoclonal antibody which specifically
CC binds to a patched protein (PTC) other than that from Drosophila. Also
CC given are the protein and coding sequences of patched from the beetle,
CC mouse, butterfly, fruit fly, mosquito and human. Patched is a segment
CC polarity gene involved in limb patterning. The sequences can be used to
CC study development and to isolate the patched ligand, hedgehog. In
CC addition, antibodies can be used to detect the PTC protein on cell
CC surfaces or to inhibit the transduction of signal by the PTC ligand by
CC competing for its binding site
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 4; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827
```

```
Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
              ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
              :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
              |:||| |   |  |||| |:|:|:||||| | ||: |:|||||| |  |:     |:
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
              :||:| ||||||||:|||   || : ::| |||||||: ||||||||:||:|||:|||||
Db       1008 SYPNGYPFFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
              ||:|| :|||||:|||||:|||||||||||||||| |||  | :| ||  |||| ||||
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
              |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139
                  ::   |||          ||                              | ||
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G------------------------------------------------------------ 1140
              |
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                            |||                ||:|
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
              :||     |:|||:||||:||   :|
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 12
AAE19830
ID AAE19830 standard; protein; 1447 AA.
XX
AC AAE19830;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human patched (Ptch) protein.
XX
KW Human; patched; Ptch; cell proliferation; differentiation; therapy;
KW cytostatic; testicular cancer; hedgehog protein signalling.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	100. .119
FT		/label= TM1
FT		/note= "Transmembrane domain"
FT	Domain	438. .458
FT		/label= TM2
FT		/note= "Transmembrane domain"
FT	Domain	471. .493
FT		/label= TM3
FT		/note= "Transmembrane domain"
FT	Domain	502. .521
FT		/label= TM4
FT		/note= "Transmembrane domain"
FT	Domain	548. .570
FT		/label= TM5
FT		/note= "Transmembrane domain"
FT	Domain	578. .599
FT		/label= TM6
FT		/note= "Transmembrane domain"
FT	Domain	751. .769
FT		/label= TM7
FT		/note= "Transmembrane domain"
FT	Domain	1028. .1048
FT		/label= TM8
FT		/note= "Transmembrane domain"
FT	Domain	1052. .1074
FT		/label= TM9
FT		/note= "Transmembrane domain"
FT	Domain	1078. .1097
FT		/label= TM10
FT		/note= "Transmembrane domain"
FT	Domain	1122. .1141
FT		/label= TM11
FT		/note= "Transmembrane domain"
FT	Domain	1155. .1178
FT		/label= TM12
FT		/note= "Transmembrane domain"

XX
PN US6348575-B1.
XX
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081884P.
XX
PA (GETH) GENENTECH INC.
XX
PI De Sauvage F, Carpenter DA;
XX
DR WPI; 2002-215260/27.
XX
PT Native human patched-2 polypeptide for treating disorders caused by
PT Hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 3; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to Hedgehog, especially
CC Desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC Hedgehog protein signalling. The present sequence is human patched (Ptch)
CC protein. Note: The sequence shown as SEQ ID NO: 4 in sequence listing of
CC the specification is a fragment of the sequence shown as SEQ ID NO: 4 in
CC fig 3 of the specification
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
                |||   |  |  ||  |     ||||||| || ||| ||| ||::||| | :||| |||
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :|| |:||:|:||
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231
```

```
Qy       189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db       232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy       248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db       292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy       308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db       352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy       367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db       411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy       427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db       471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy       485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db       531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy       545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db       591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy       596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db       651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy       645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db       711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy       705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db       769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy       765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
Db       828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy       825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
Db       888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy       885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
Db       948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy       944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
Db      1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy      1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
Db      1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy      1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db      1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy      1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139
Db      1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy      1140 G------------------------------------------------------------ 1140
Db      1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy      1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
```

```
                                                    |||                 ||:|
Db      1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy      1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db      1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 13
ABJ10931
ID ABJ10931 standard; protein; 1447 AA.
XX
AC ABJ10931;
XX
DT 12-DEC-2002 (first entry)
XX
DE TRC8 related human patched protein SEQ ID No 5.
XX
KW TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3,2;
KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
KW human chromosomal translocation.
XX
OS Homo sapiens.
XX
PN US2002106656-A1.
XX
PD 08-AUG-2002.
XX
PF 02-JUL-2001; 2001US-00898533.
XX
PR 12-MAR-1998; 98US-0077723P.
PR 12-MAR-1999; 99US-00268140.
XX
PA (GEMM/) GEMMILL R M.
PA (DRAB/) DRABKIN H A.
XX
PI Gemmill RM, Drabkin HA;
XX
DR WPI; 2002-712395/77.
XX
PT Novel Translocation in Renal cancer from Chromosome 8 genes, useful for
PT detection of tumors, comprises rearrangements in the t(3;8)(p14.2;q24.1)
PT chromosomal translocation which occurs in renal and thyroid carcinomas.
XX
PS Disclosure; Fig 2D; 49pp; English.
XX
CC The invention relates to an isolated TRC8 (Translocation in Renal cancer
CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
CC comprising a sequence of 664 amino acids fully defined in the
CC specification and comprising a sequence located in the 5' flanking region
CC to the coding region of TRC8 and a sequence which occurs in certain
CC sporadic renal cell carcinomas. The methods are useful for detecting the
CC presence of the TRC8 gene in a biological sample, detecting alterations
CC to the gene, such as a 3;2 human chromosomal translocation, and fused DNA
CC containing the fused site of TRC8/FHIT. A nucleic acid probe is useful
CC for detecting the 3;8 human chromosomal translocation, by contacting the
CC nucleic acid probe with a biological sample to be tested, and determining
CC whether the nucleic acid probe specifically hybridises to the TRC8FHIT or
CC FHIT/TRC8 fusion DNA. This sequence represents a TRC8 related protein of
CC the invention
XX
SQ Sequence 1447 AA;

  Query Match   53.4%; Score 3348; DB 5; Length 1447;
  Best Local Similarity 49.9%; Pred. No. 1.5e-291;
  Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps   18;

```
Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
```

```
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188

Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247

Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307

Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366

Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426

Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484

Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544

Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595

Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644

Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704

Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764

Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824

Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884

Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943

Db        948 WVHDKADYMPETRLRIPAAEPIEYAQFPPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003

Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063

Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121

Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP-----------------------------APQGG 1139

Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G---------------------------------------------------------- 1140

Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155

Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

RESULT 14
AAG79571
ID AAG79571 standard; protein; 1447 AA.
XX
AC AAG79571;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human patched protein.
XX
KW Patched; ptc; basal cell nevus syndrome; BCNS; wound healing;
KW developmental disorder; spina bifida; craniofacial abnormality;
KW basal cell carcinoma; skin; brain tumour; transgenic; mouse;
KW proliferation; oncogenesis; signal transduction; cancer; aging.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 113
FT   /note= "Encoded by CCG"
FT Misc-difference 413
FT   /note= "Encoded by GAG"
FT Misc-difference 864
FT   /note= "Encoded by GAA"
XX
PN US6429354-B1.
XX
PD 06-AUG-2002.
XX
PF 22-AUG-1997; 97US-00918658.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
PR 31-MAY-1996; 96US-00656055.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (REGC) UNIV CALIFORNIA.
XX
PI Scott MP, Goodrich LV, Johnson RL, Epstein E;
XX
DR WPI; 2002-722086/78.
DR N-PSDB; ABA00374.
XX
PT Transgenic mouse, useful for cancer drug screening, comprises disruption
PT of allele of patched locus which predisposes the mouse to develop a
PT proliferative disorder.
XX
PS Disclosure; Col 85-92; 58pp; English.
XX
CC This sequence shows human patched (ptc) protein. Human patched gene has
CC been mapped to human chromosome band 9q22.3 and lies between two
CC polymorphic makers D9S196 and D9S287. Mutations in the patched gene are
CC characteristic in basal cell nevus syndrome (BCNS), an inherited disorder
CC with an increased risk of developmental disorders such as spina bifida
CC and craniofacial abnormalities, basal cell carcinoma of the skin and
CC brain tumours. The human and mouse ptc sequences show 86% homology. The
CC transgenic mouse of the invention has a genome comprising a disruption of
CC at least one allele of a patched locus, where the disruption predisposes
CC the mouse to develop a proliferative disorder. The transgenic mouse is

```
CC   useful for studying patched function and regulation, for e.g. a series of
CC   small deletions and/or substitutions made in the patched gene, to
CC   determine the role of different exons in oncogenesis, signal
CC   transduction, etc; and for drug screening which is useful for treating
CC   cancer or developmental abnormalities attributed to a defect in patched
CC   function such as wound healing and aging
XX
SQ   Sequence 1447 AA;

  Query Match           53.4%;  Score 3348;  DB 5;  Length 1447;
  Best Local Similarity   49.9%;  Pred. No. 1.5e-291;
  Matches  672;  Conservative  203;  Mismatches  285;  Indels  186;  Gaps   18;

Qy         12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db         53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy         69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
Db        112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy        129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
Db        172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy        189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
Db        232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy        248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
Db        292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy        308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
Db        352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy        367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
Db        411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy        427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db        471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy        485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db        531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy        545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
Db        591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy        596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
Db        651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy        645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
Db        711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy        705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db        769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy        765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
Db        828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWQTGKIMPNNYKNGSDDGVLAYKLL 887

Qy        825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
Db        888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy        885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
Db        948 WVHDKADYMPETRLRIPAAEPIEYAQPFPYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy        944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
Db       1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy       1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
Db       1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy       1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db       1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy       1122 ----QMYKESPE-------ILSPP------------------------------APQGG 1139
Db       1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy       1140 G---------------------------------------------------------- 1140
Db       1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy       1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
Db       1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy       1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db       1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

```
RESULT 15
ABU62275
ID   ABU62275 standard; protein; 1447 AA.
XX
AC   ABU62275;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Human patched gene PTC product.
XX
KW   Human; patched gene; PTC; hedgehog protein; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003032085-A1.
XX
PD   13-FEB-2003.
XX
PF   20-OCT-1997;   97US-00954701.
XX
PR   07-OCT-1994;   94US-00319745.
PR   06-OCT-1995;   95US-00540406.
XX
PA   (SCOT/) SCOTT M P.
PA   (GOOD/) GOODRICH L V.
PA   (JOHN/) JOHNSON R L.
XX
PI   Scott MP,  Goodrich LV,  Johnson RL;
XX
DR   WPI; 2003-492065/46.
XX
PT   New DNA sequence other than present in a chromosome encoding patched gene
PT   other than Drosophila patched gene, useful for preparing transgenic
PT   laboratory animals and to knock out patched protein in embryonic stem
PT   cells.
XX
PS   Disclosure; Page 8-10; 40pp; English.
XX
CC   The invention relates to a DNA sequence other than present in chromosome
CC   encoding a patched (ptc) gene other than Drosophila patched gene. A cell
```

CC expressing the DNA sequence is useful for producing patched protein, by
CC growing the cell expressing the DNA sequence, where the patched protein
CC is expressed and isolating the patched protein free of other proteins.
CC The cell expressing the DNA sequence is also useful for screening
CC candidate compounds for binding affinity to the patched protein, by
CC combining the candidate protein with the cell expressing the DNA sequence
CC where the DNA sequence comprises the entire coding sequence under the
CC transcriptional regulation of the transcriptional initiation region and a
CC transcriptional termination region functional in the cell, expressing the
CC patched protein in the cell and assaying for the binding of the candidate
CC compound to the patched protein. The above cell is useful for screening
CC candidate compounds for agonist activity with the patched protein. The
CC DNA sequence is useful for producing all or portions of the patched
CC protein, as probes for research, diagnosis, binding of hedgehog protein
CC for its isolation and purification and in gene therapy. The DNA sequence
CC is also useful as primers for investigating other species and for
CC isolating genes from various mammalian sources of interest, particularly
CC from humans or from domestic animals. The DNA sequence is further useful
CC for preparing transgenic laboratory animals and to knock out the PTC
CC protein in the embryonic stem cells, so as to produce hosts with single
CC functional patched gene. The present sequence represents the amino acid
CC sequence of the human patched gene PTC product
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 7; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

```
Qy          12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
               |||   |  |  ||  |     |||||||| || ||| ||| ||::||| | :||| |||
Db          53 PSYC-DAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGA 111

Qy          69 LALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEEAAYTSQMLIQTARQEGENILT 128
               |:||: | :|||:|:|||||| |||:||:||::|:|||| :  |::||| ::|| |:||
Db         112 FAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171

Qy         129 PEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTP 188
               |||  || :|| ||:| | :| : | |  :|||||  : | | :: :: :|| |:|||:|:||
Db         172 TEALLQHLDSALQASRVHVYMYNRQWKLEHLCYKSGELITETGYMDQIIEYLYPCLIITP 231

Qy         189 LDCFWEGAKLQGGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELLDKAQVGQAY 247
               |||||||||| |:||| |:| ::||| || : ||||      :: : |:|:||:||  |
Db         232 LDCFWEGAKLQSGTAYLLGKPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291

Qy         248 VGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDPQ 307
               : ||||:| |  || :||| :| :  ::|  |:||||| | |:|||||::||  ::
Db         292 MDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNST 351

Qy         308 GELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
               |:|: | |||: | ||:|:|:||||:| :| :| | |:|::|: :|:|||| :|::  ::
Db         352 GKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAWQRTYVEVVHQS 410

Qy         367 LPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQGSVG 426
               : :|::|:: :|::|||||| :||:||  ||  |||||||||:|||||::|||:||
Db         411 VAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRWDCSKSQGAVG 470

Qy         427 LAGVLLVALAVASGLGLCALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
               |||||||||:||:|||||:|:||:|||||||||||||:||||||||||:|
Db         471 LAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAFSETGQNKR 530

Qy         485 TPLQERMGECLQRTGTSVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
               | ::| ||||:||| || ||||:|: || ||||:|||||||||||:||   |  |:|
Db         531 IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLL 590

Qy         545 VFPAILSLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGD-------GTVPVGIAH-- 595
               :||||||:|| ||  :|||: |||:||| ::|||: ||   |          |   :|
Db         591 IFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHSF 650

Qy         596 -------LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGSELFSPGGSTRD 644
                    : :|||  |  :  :   |   |:: :   |     | |  :      ||||
Db         651 AHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSCQSPESTSSTRD 710

Qy         645 LLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLSLYGA 704
               || |  ::     |  || :| }: ||   :|| ||:  || :|: ||  |||:||||
Db         711 LLSQFSDS--SLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLGVSLYGT 768

Qy         705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
               | |:||| |||:||| |:|: |::|| :||| | : :|||   || : |  |:|||: ||
Db         769 TRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827

Qy         765 SLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLL 824
               ::| |:     | |: ||||:|:||||:| ||| || :|:|  ::|:|||:|| ||||||
Db         828 NVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLL 887

Qy         825 IQTGDAQEPLDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPPE 884
               :|||   :|:| |||| ::||| :|:| |  ||: || |||:||:  ||||||  |  ||
Db         888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRPE 947

Qy         885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVH 943
               |:||| |   |  |||| |:|:|:||||| | ||: |:|||||||  |  |:     |:
Db         948 WVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007

Qy         944 AYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMTVEL 1003
               :||:| ||||||||:|||   || : ::| |||||||: |||||||||:||:|||:|||||
Db        1008 SYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMVLALMTVEL 1067

Qy        1004 FGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLRAAHALEHTFAPVT 1063
               ||:|| :||||||:|||||:|||||||||||||| ||| | :| ||  |||| ||||
Db        1068 FGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127

Qy        1064 DGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
               |||:|||||:|||||| |||||||||| | :||:||:|:|||||||||  || |||
Db        1128 DGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPA 1187

Qy        1122 ----QMYKESPE-------ILSPP-------------------------------APQGG 1139
                   ::   |||          ||                                | ||
Db        1188 NGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQGA 1247

Qy        1140 G------------------------------------------------------------ 1140
               |
Db        1248 GGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQGQQPRRDPP 1307

Qy        1141 ----------------------------LRWG----------------ASSSLPQSFAR 1155
                                           |||                 ||:|
Db        1308 REGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQP 1367

Qy        1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
               :||     |:|||:||||:||   :|
Db        1368 ITTVTASASVTVAVHPPPVPGPGRNP 1393
```

Search completed: November 22, 2004, 07:55:54
Job time : 89 secs